JRC SCIENCE FOR POLICY REPORT

a4a short research project Spatial effects on the stock dynamics of European Atlantic sardine stocks

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2016

EUR 27841 EN

Joint
Research
Centre

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Spatial effects on the stock dynamics of European Atlantic sardine stocks

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JRC Science Hub
https://ec.europa.eu/jrc

JRC101074

EUR 27841 EN

ISBN 978-92-79-57759-8

ISSN 1831-9424

doi:10.2788/890201

Luxembourg: Publications Office of the European Union, 2016

Contents

Abstract

Under the scope of the a4a Initiative a workshop dedicated to studying spatial effects on the stock dynamics of European Atlantic sardine took place in Ispra, Italy, the 14th to the 18th of December 2015, with the objectives of (i) explore a4a methods to assess the Southern sardine stock (Atlanto-Iberian stock) and compare the results with the current ICES assessment carried out with SS3; (ii) explore a4a methods to assess the Northern stock of sardine stock; and (iii) apply a4a to assess putative sub-stock units; discuss local depletion and mixing among sub-units of the stock. Sardine is fished mainly by UK, Netherlands France, Spain and Portugal across ICES areas VII, VIII and IXa. In France, Spain and Portugal sardine has significant social and economic importance to the fishing and canning industries. Sardine shows a complex population structure characterized by spatial heterogeneity in phenotypic characters and life-history traits. Evidence of spatial variability in dynamics does not preclude some fish mixing across the whole region, in agreement with both genetic homogeneity and the similarity in otolith element composition in larger fish. Current knowledge on sardine biology and dynamics is consistent with the hypothesis of a meta-population composed of three populations recruiting in the Bay of Biscay, off northern Portugal, and in the Gulf of Cadiz. The workshop looked into three options of spatial structures (i) current stock structure Bay of Biscay stock (BB; VIIIa,b) and Ibero Atlantic stock (IB; IXa and VIIIc); (ii) three separate sub-units Bay of Biscay, Northwest stock (NW; VIIIc, IXa-North to IXa-Central South) and South stock (S; IXa South); and (iii) a single stock. The a4a stock assessment model was used to estimate the dynamics of each sub-units in each option. To carry out the comparison across sub-units the models used were kept as similar as possible, to mitigate the effect that the choice of model can have on the final results. Uncertainty was estimated using MCMC with the ADMB implementation, which, in the most recent version, can be assessed through the FLa4a package. In the case of the overall stock, a sensitivity analysis about survey's data processing options was carried out, to investigate the robustness of the assessment results. For the Bay of Biscay a bayesian approach has also been implemented. In order to compare both methods (a4a and bayesian) a very simple separable model was selected. A visual evaluation of the consistency between the spatial hypothesis was done based on the SSB estimates, showing that both trends are remarkably similar until 2012, when they start to diverge. In 2012 the Iberian stock (sub-units NW and S) was at a very low level and the migration rates between the Iberian and the Bay of Biscay sub-units may have increased. In such case, the stock assessment model assumption of closed population is less likely to be maintained and the two estimates of SSB diverge. One of the advantages of the approach proposed is to make it possible to look into sub-units of the stock with regards to their productivity and exploitation. These results are shown as time series of fishing mortality and recruitment for each sub-unit.

Acknowledgements

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1. Introduction

Under the scope of the a4a Initiative, the JRC is promoting cooperative activities with the aim to test, disseminate and promote a4a methods. These Small Research Projects (SRP) are focus on comparing the results of assessments from other models to assessments obtained from the a4a statistical catch-at-age model, and explore research questions using case studies.

The Workshop dedicated to studying spatial effects on the stock dynamics of European Atlantic sardine took place in Ispra, Italy, the 14th to the 18th of December 2015, with the following objectives:

- Explore a4a to assess the Southern sardine stock (Atlanto-Iberian stock) and compare the results with the current ICES assessment carried out with SS3.
- Explore a4a to assess the Northern sardine stock.
- Apply a4a to assess putative sub-stock units; discuss local depletion and mixing among sub-units.

1.1 ToRs and Agenda

The terms of reference of the workshop were:

1. Use the a4a stock assessment framework to study spatial effects on stock dynamics of sardine in European Atlantic waters.
2. Compare results with other stock assessment methods.

The first day of the workshop was dedicated to a brief presentation of a4a, discussion of stock structure hypotheses and finalize the preparation of datasets. Taking into account the spatial dynamics of sardine in European waters, the level of data disaggregation and time available, participants agreed to explore the following stock structure scenarios:

- S0: Current stock structure: Bay of Biscay stock (BB; VIIIa,b) and Ibero Atlantic stock (IB; IXa and VIIIc);
- S1: Three separate stocks: Bay of Biscay, Northwest stock (NW; VIIIc, IXa-North to IXa-Central South) and South stock (S; IXa South);
- S2: Single stock formed by the three components in S1.

Methods were discussed the second day. The remaining days were dedicated to run assessments and discuss results.

1.2 The a4a Initiative

The volume and availability of data useful for fisheries stock assessment is continually increasing. Time series of traditional sources of information, such as surveys and landings data are not only getting longer, but also cover an increasing number of species.

For example, in Europe the 2009 revision of the Data Collection Regulation (EC, 199/2008) has changed the focus of fisheries sampling programmes away from providing data for individual assessments of key stocks (i.e. those that are economically important) to documenting fishing trips, thereby shifting the perspective to a large marine monitoring programme. The result has been that data on growth and reproduction of fish stocks are being collected for more than 300 stocks in waters where the European fleets operate.

Recognizing that the context above required new methodological developments, the European Commission Joint Research Centre (JRC) started its Assessment for All Initiative

(a4a), with the aim to develop, test, and distribute methods to assess large numbers of stocks in an operational time frame, and to build the necessary capacity/expertise on stock assessment and advice provision.

The long-term strategy of a4a is to increase the number of stock assessments while simultaneously promoting the inclusion of the major sources of uncertainty in scientific advice. The tactic is to reduce the required workload by developing a software framework with 'simple' methods required to run assessments (Jardim, et.al, 2014), including methods to deal with recognized bottlenecks, *e.g.* model averaging to deal with model selection (Millar, et.al, 2014). Moreover, this framework makes the analysis more intuitive, thereby attracting more experts to join stock assessment teams. Having more scientists/analysts working in fisheries management advice will increase the human resource basis, which is currently recognized to be limited. Regarding the former, a4a promotes a risk analysis approach to scientific advice through a wider usage of Operating Model/MSE approaches. a4a is focused on developing methods that can deal with the most common settings these type of analysis require, and create the conditions for scientists to develop their own methods. The expectation is that having a common framework, with clear data structures and workflows, will promote research in this area and make it simpler to implement and share methods.

To achieve these objectives, the Initiative identified a series of tasks, which were or are being carried out, namely:

- define a moderate data stock;
- develop a stock assessment framework;
- develop a forecasting algorithm based on MSE;
- organize training courses for marine scientists.

1.3 The a4a approach to stock assessment and management advice

As stated before, one of the main objectives of a4a is to promote a risk type of analysis, so that scientific advice provides policy and decision makers a perspective of the uncertainty existing on stock assessments and its propagation into the scenarios being analyzed.

The sources of uncertainty implemented so far are related to the processes of growth, natural mortality and reproduction (stock-recruitment); and to the estimation of population abundance and fishing mortality. In all cases the framework can include sampling error.

The approach is split into 4 steps: (i) converting length data to age data using a growth model, (ii) modeling natural mortality, (iii) assessing the stock, and (iv) MSE.

These steps may be followed in sequence or independently, depending on the user's preferences. All that is needed is to use the objects provided by the previous step and provide the objects required by the next, so that data flows between steps smoothly. One can make the analogy with building with Lego, where for each layer the builder may use the pieces provided by a particular boxset, or make use of pieces from other boxsets. Figure 1 shows the process, including the class of the objects that carry the data (in black).

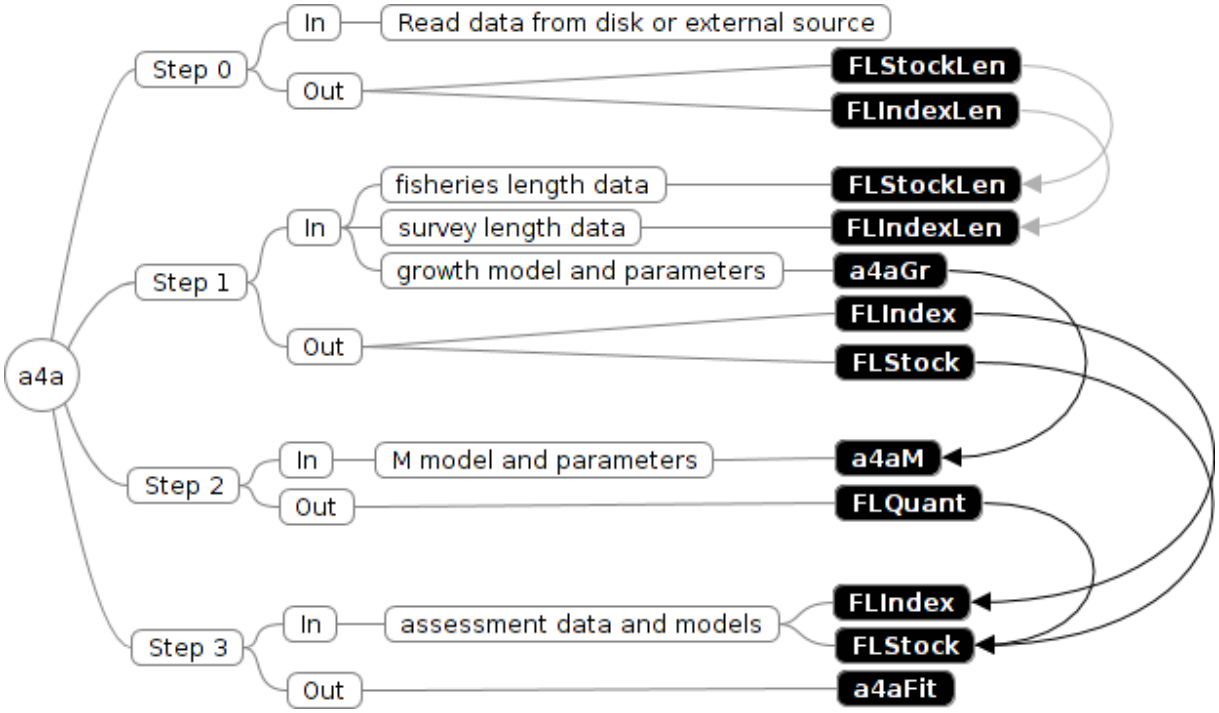

Figure 1: In/out process of the a4a approach. The boxes in black represent the classes of the objects that carry the information in and out of each step.

Analysis related to projections and biological reference points are dealt with by the `FLR` packages `FLash` and `FLBRP`.

In Steps 1 and 2 there is no fitting of growth models or natural mortality models. The rationale is to provide tools that allow the uncertainty associated with these processes to be carried on into the stock assessment, e.g. through parameter uncertainty. This approach allows the users to pick up the required information from other sources of information such as papers, PhDs, Fishbase, other stocks, etc. If the stock under analysis does not have specific information on the growth or natural mortality processes, generic information about life history invariants may be used such as the generic priors suggested by Bentley, (2014).

Note that an environment like the one distributed by a4a promotes the exploration of different models for each process, giving the analyst a lot of flexibility. It also opens the possibility to efficiently include distinct models in the analysis. For example, a stock assessment using two growth, or several models for natural mortality could be performed. Our suggestion to streamline the assessment process is to combine the final outcomes using model averaging (Miller, et. al, 2014). Other solutions may be implemented, like scenario analysis, etc. What is important is to keep the data flowing smoothly and the models clear. R (R Core Team, 2014) and `FLR` (Kell, et.al, 200) provide powerful platforms for this approach.

1.4 How to read this document

The target audience for this document are marine scientists, in particular stock assessment experts. It presents a mixture of text and code that shows how the analysis can be run with `R/FLR/FLa4a`. The chapters are as independent as possible, so they can be extracted and run individually.

1.5 Software packages - FLR & FLa4a

To run the `FLa4a` methods the reader will need to install the package and its dependencies and load them, together with a couple of other packages. The data sets can be made available upon request.

```
# from CRAN
install.packages(c("copula", "triangle", "coda"))
# from FLR
install.packages(c("FLCore", "FLa4a"), repos = "http://flr-project.org/R")
```

To replicate the analysis carried out in this document the user will need the following additional packages:

```
# from CRAN
install.packages(c("plyr", "xtable", "plot3D", "gridExtra", "ggplot2"))
# from FLR
pkgs <- c("FLXSA", "FLAssess", "FLSAM", "FLash", "FLBRP")
install.packages(pkgs, repos = "http://flr-project.org/R")
```

After installing the reader will have to load the packages into one's R session.

```
library(coda)
library(FLa4a)
library(ggplotFL)
library(plyr)
library(grid)
source("funs.R")
trellis.par.set("strip.background", list(alpha = 1, col = "gray90"))
```

2. The sardine fishery in the European Atlantic EEZ

Sardine is fished mainly by UK, Netherlands France, Spain and Portugal across ICES areas VII, VIII and IXa (Silva *et.al*, 2015). In France, Spain and Portugal sardine has significant social and economic importance to the fishing and canning industries. Two stocks of sardine, Northern and Southern, are considered in the European Atlantic EEZ.

Sardine from the Northern stock is fished mainly by France and Spain (90% of annual landings) in ICES Area VIII (Figure 2). The French fishery of sardine is carried out by 30 purse seiners and 10 pair trawlers. Purse seiners target sardine in coastal areas (<10 nautical miles) all year round with a seasonal peak in summer, and make 80% of total sardine catches. Pair-trawlers may operate until 50 nautical miles offshore and are more opportunistic in relation to their targets. The Spanish fleet licensed to fish sardine in Division VIIIb has about 100 purse seiners which target sardine in the Spring and Autumn. Preliminary estimates indicate about 1200 fishermen are employed in the fleets fishing sardine. Total French and Spanish landings in 2014 were 40000 tonnes corresponding to 41 MEuro[1] at first sale. Landings doubled since 1990 due to high sardine abundance in the area, increasing interest of the French fleets and, more recently, of the Spanish fleet due to the low abundance and catch opportunities in the Iberian stock. Smaller catches are irregularly produced in subarea VII by fleets of several countries, mainly France, UK and Netherlands.

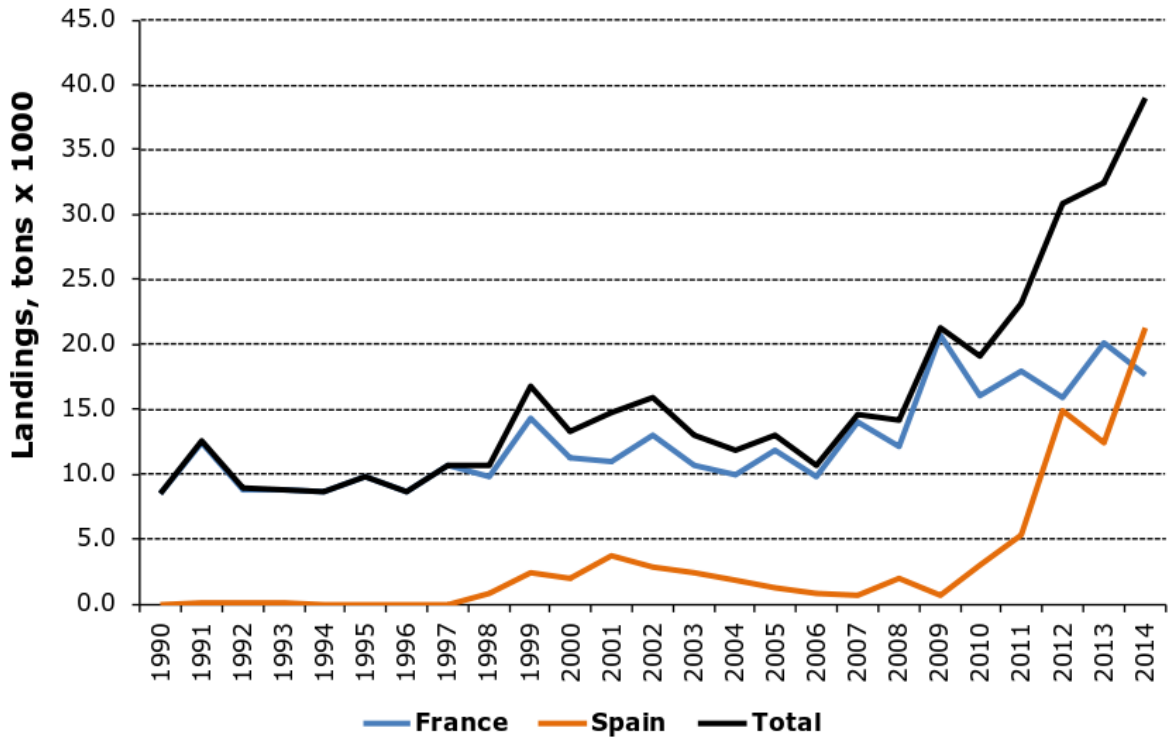

Figure 2: Historical series of sardine landings by country from the Northern stock (ICES area VIII).

Sardine from the Southern stock is fished by the purse seine fleets of Spain and Portugal in continental shelf waters (Figure 3). In 2014, the Spanish fleet had 364 vessels, 77% targeting sardine and operating in the Cantabrian and Northwestern waters. The remaining vessels operate in the Gulf of Cadiz, target anchovy and catch sardine in certain periods of the year. The Portuguese fleet has 180 vessels targeting sardine. Preliminary estimates indicate about 5700 fishermen are employed in the two fleets. The total Spanish and

[1] 10^6 euros

Portuguese landings in 2014 were 27900 tonnes corresponding to 47 MEuro[2] at first sale. Landings show a decreasing trend since 1981; a sharp decrease of 65%, (80400 tonnes to 27900 tonnes) took place between 2011 and 2014 due to the decline of the stock and catch regulations. Sardine is the main product of the fish canning industry in Portugal: 20 canning factories with ca.3500 workers produced 13000 t (54 MEuro[3]) of canned sardine in 2014 mostly for export. In Spain, the fish canning production is more diverse. In Galicia (Northwest of Spain), where 80% of the fish caning industry is located, there are 65 canning factories with over 12000 employees. The annual production of canned sardine is estimated to be higher than 22000 tonnes, mostly for export.

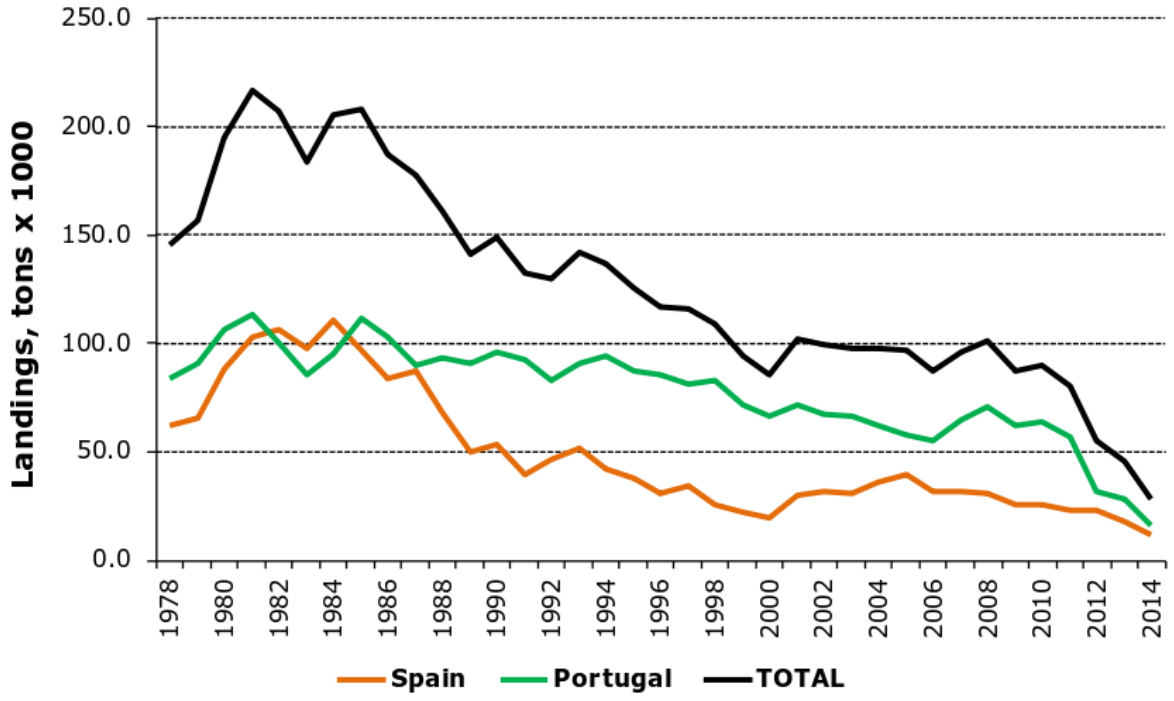

Figure 3: Historical series of sardine landings by country from the Southern stock (ICES sub-area VIIIc and IXa)

[2] 10^6 euros
[3] 10^6 euros

3. The spatial dynamics of the sardine stocks

Sardine recruitment is localized in a few areas off the Iberian Peninsula and Bay of Biscay: the southern part of the Bay of Biscay and off southern Britanny, off Lisbon (southwest Portugal), over a wide coastal area off northern Portugal, and across a large part of the Gulf of Cadiz shelf (see Silva *et.al*, 2009, and references therein). These recruitment "hotspots" coincide with areas of significant river discharge and, therefore, high productivity in winter/spring, when most spawning takes place.

Recruitment variability is generally asynchronous among hotspots, although some recruitment peaks are noticeable across wide regions. There is some indirect evidence that recruits in a given area migrate throughout their life span, although the main migration directions change over time. Figure 4 depicts recruitment hotspots and potential migration patterns. Such geographic differences in recruitment trends, coupled with migrations, are the cause of distinct trends in abundance observed in each area.

These findings are consistent with a complex population structure characterized by spatial heterogeneity in phenotypic characters and life-history traits. Evidence of spatial variability in dynamics does not preclude some fish mixing across the whole region, in agreement with both genetic homogeneity and the similarity in otolith element composition in larger fish. Current knowledge on sardine biology and dynamics is consistent with the hypothesis of a meta-population composed of three populations recruiting in the Bay of Biscay, off northern Portugal, and in the Gulf of Cadiz.

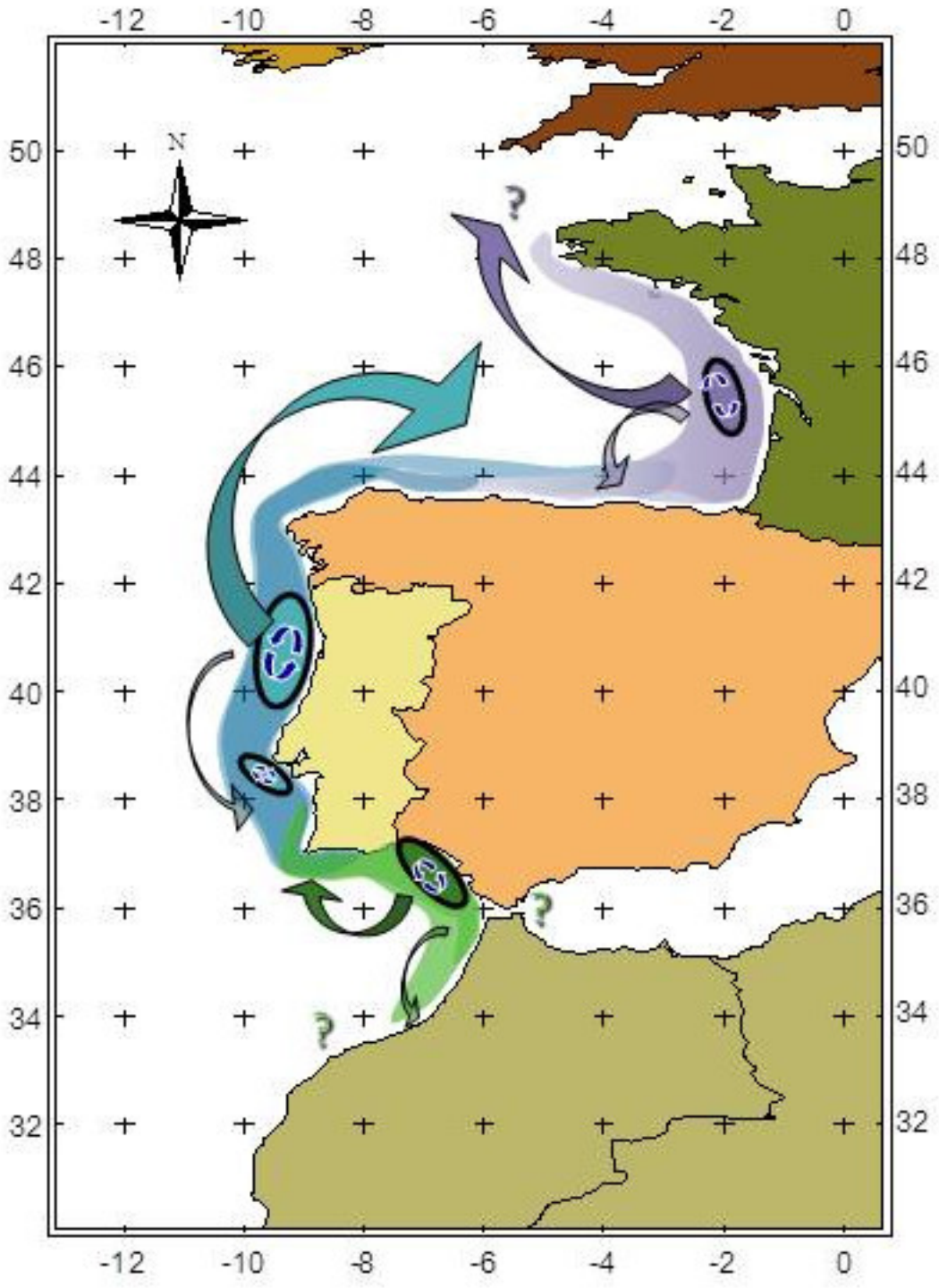

Figure 4: Spatial dynamics of sardine in the Northeast Atlantic)

4. Current stock definitions

ICES (2012) considered two sardine stock units in EU Atlantic waters (Figure 5):

- the Northern stock, distributed between the English Channel, Celtic Sea and the French-Spanish border in Bay of Biscay (ICES Area VII and Divisions VIIIa,b,d), and
- the Southern stock, also referred to as "Iberian stock", distributed south of the French-Spanish border in Bay of Biscay, to the Gibraltar Strait in the Gulf of Cadiz (ICES Divisions VIIIc and IXa).

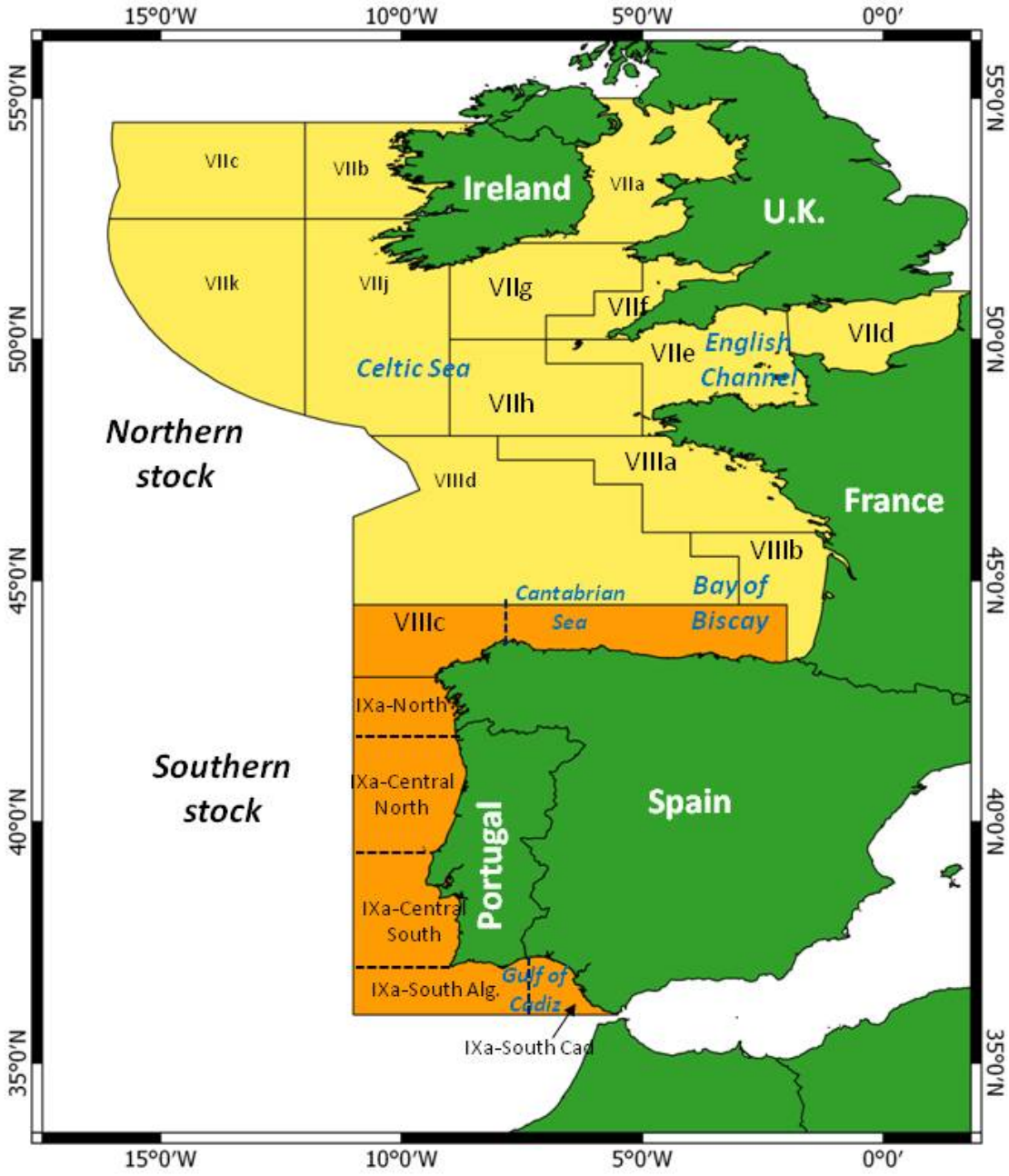

Figure 5: Sardine stocks in the Northeast Atlantic

4.1 Iberian stock

This section uses the a4a stock assessment framework to replicate, as close as possible, the official assessment, which is carried out with SS3. The objective of having a model

setting that mimics the official assessment is to facilitate a future implementation of a full feedback MSE. The input data are taken from ICES, (2015) .

4.1.1 Replicating the official assessment (SS3) with a4a

```
load("../analysis/IB/IB.Rdata")
# stock file with SS3 output
SS3.fit <- IB.stk
```

```
fmod <- ~s(replace(age, age %in% c(3:5), 3), k = 4, by = breakpts(year,
    1991)) + s(year, k = 20)
qmod <- list(~s(replace(age, age %in% c(2:5), 2), k = 3), ~1)
IB.q0f <- a4aSCA(IB.stk, IB.idx, fmodel = fmod, qmodel = qmod)
IB.q0r <- residuals(IB.q0f, IB.stk, IB.idx)
IB.q0s <- IB.stk + simulate(IB.q0f, 500)
IB.q0mc <- a4aSCA(IB.stk, IB.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
IB.q0mcmc <- as.mcmc(IB.q0mc)
IB.q0smc <- IB.stk + IB.q0mc
```

```
plot(IB.q0r)
```

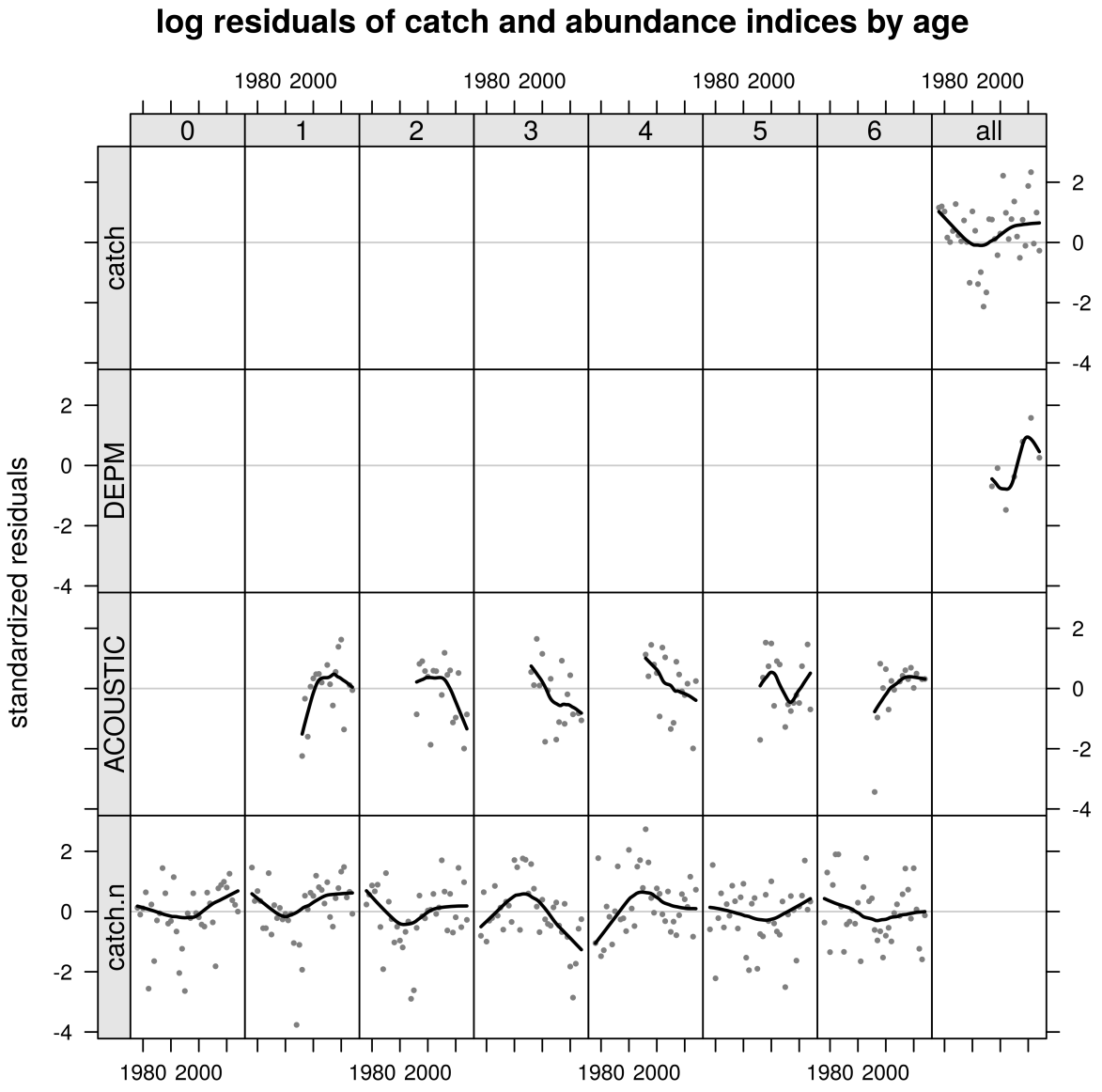

Figure 6: Residuals

```
plot(IB.q0f, IB.stk)
```

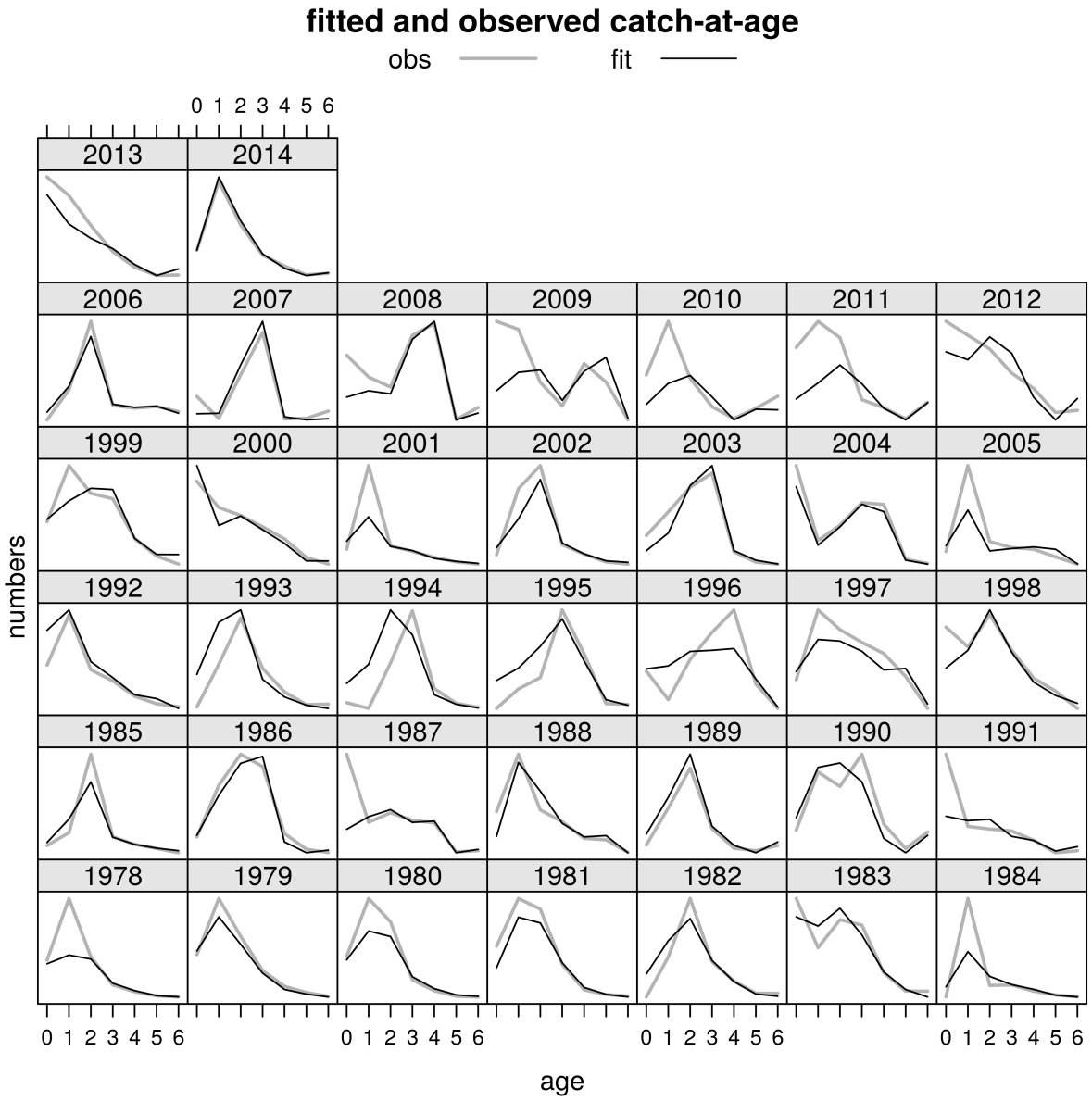

Figure 7: Catch-at-age predictions and observations

```
plot(IB.q0f, IB.idx[1])
```

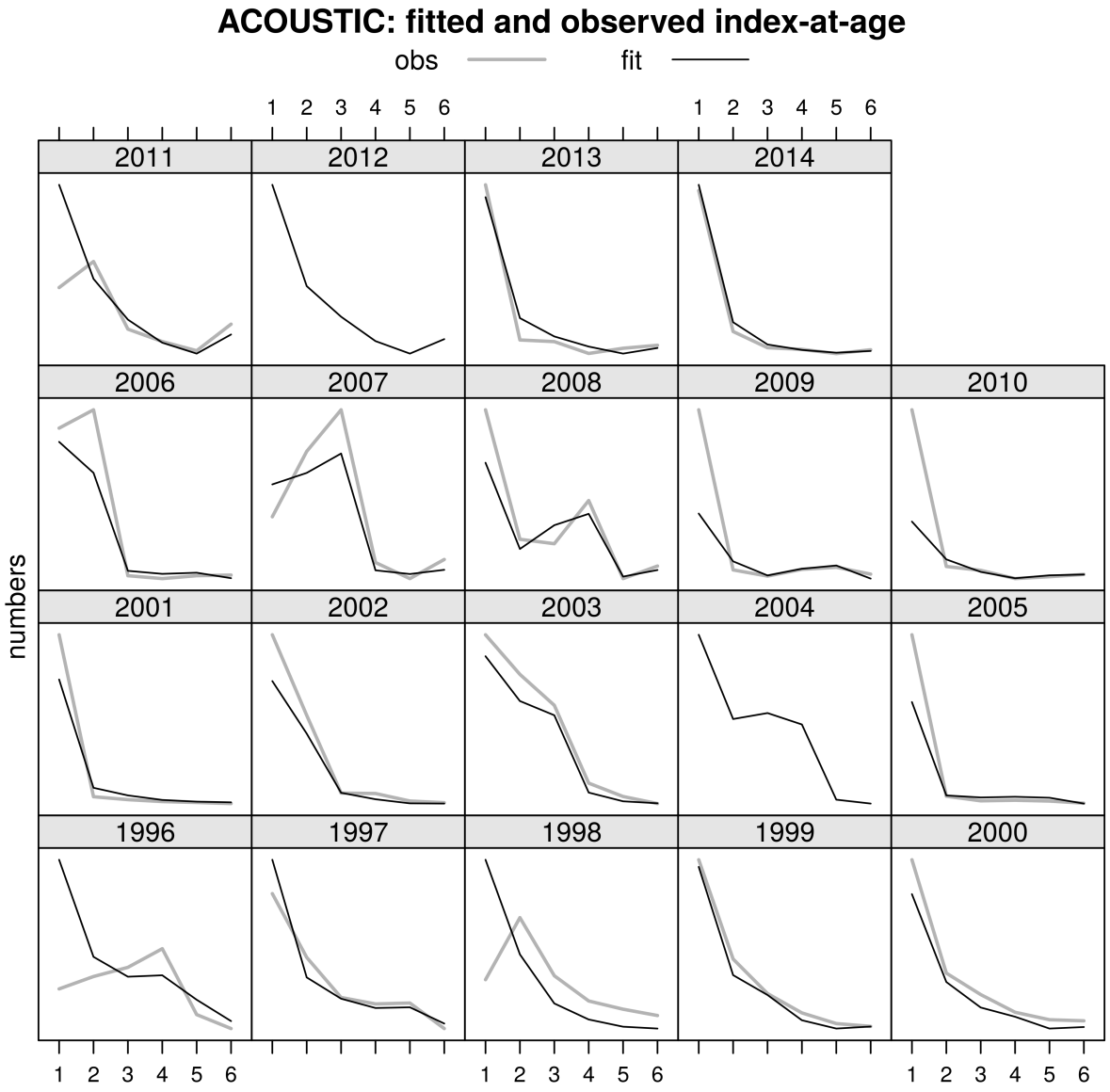

Figure 8: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(IB.q0f))
```

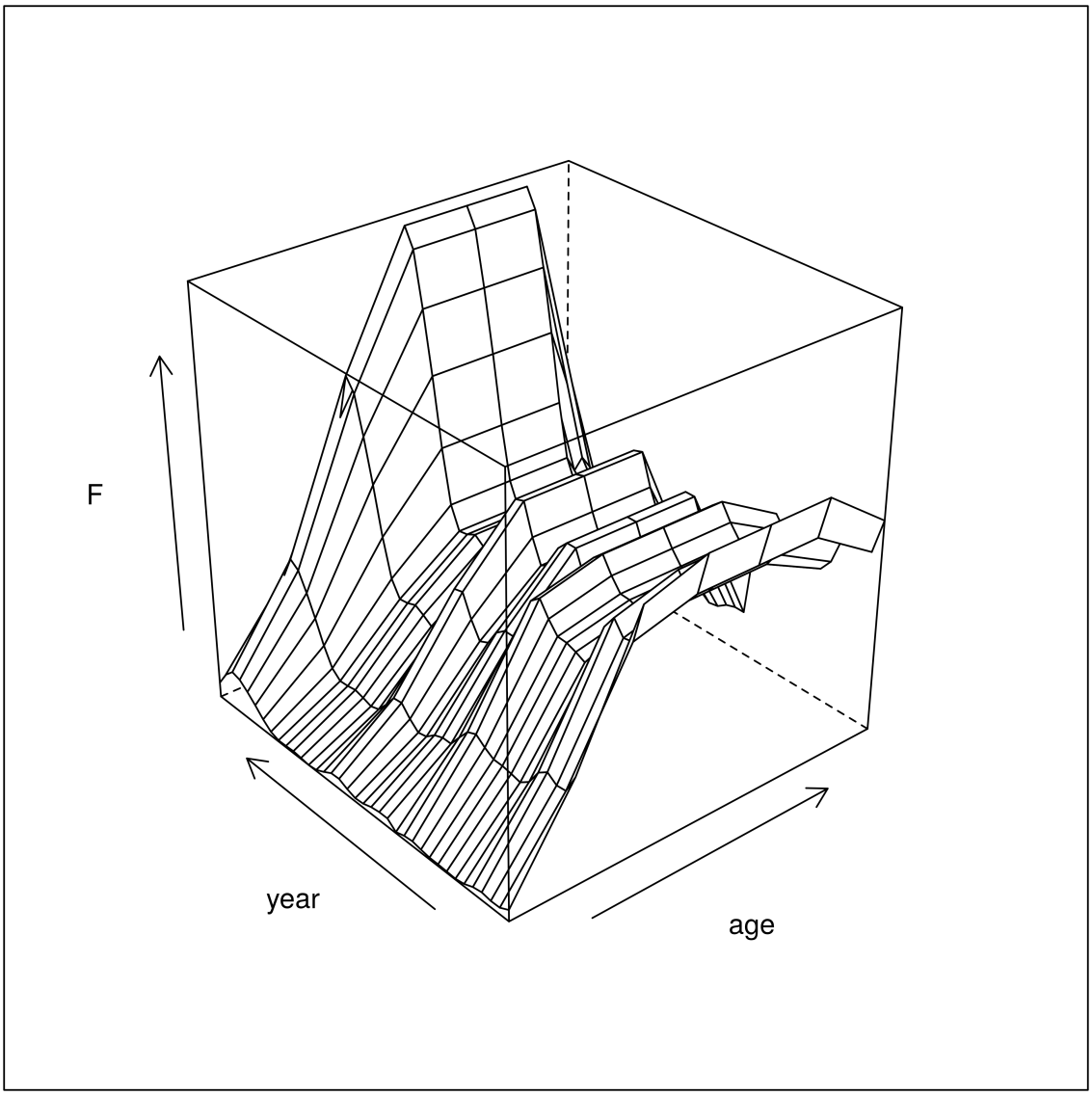

Figure 9: F-at-age estimate

```
plot(IB.q0mc)
```

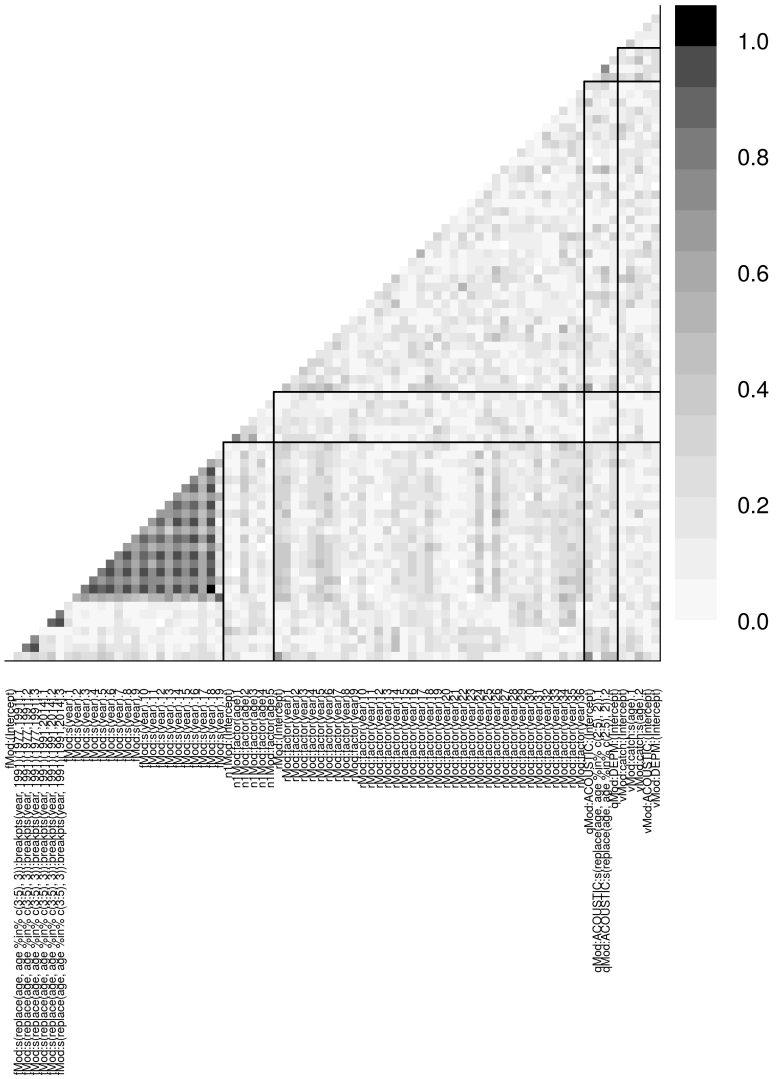

Figure 10: Absolute correlation between pairs of parameters. The blocks identify sub-models and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of two distinct sub-models

```
plot(FLStocks(a4a = IB.q0smc, ss3 = SS3.fit))
```

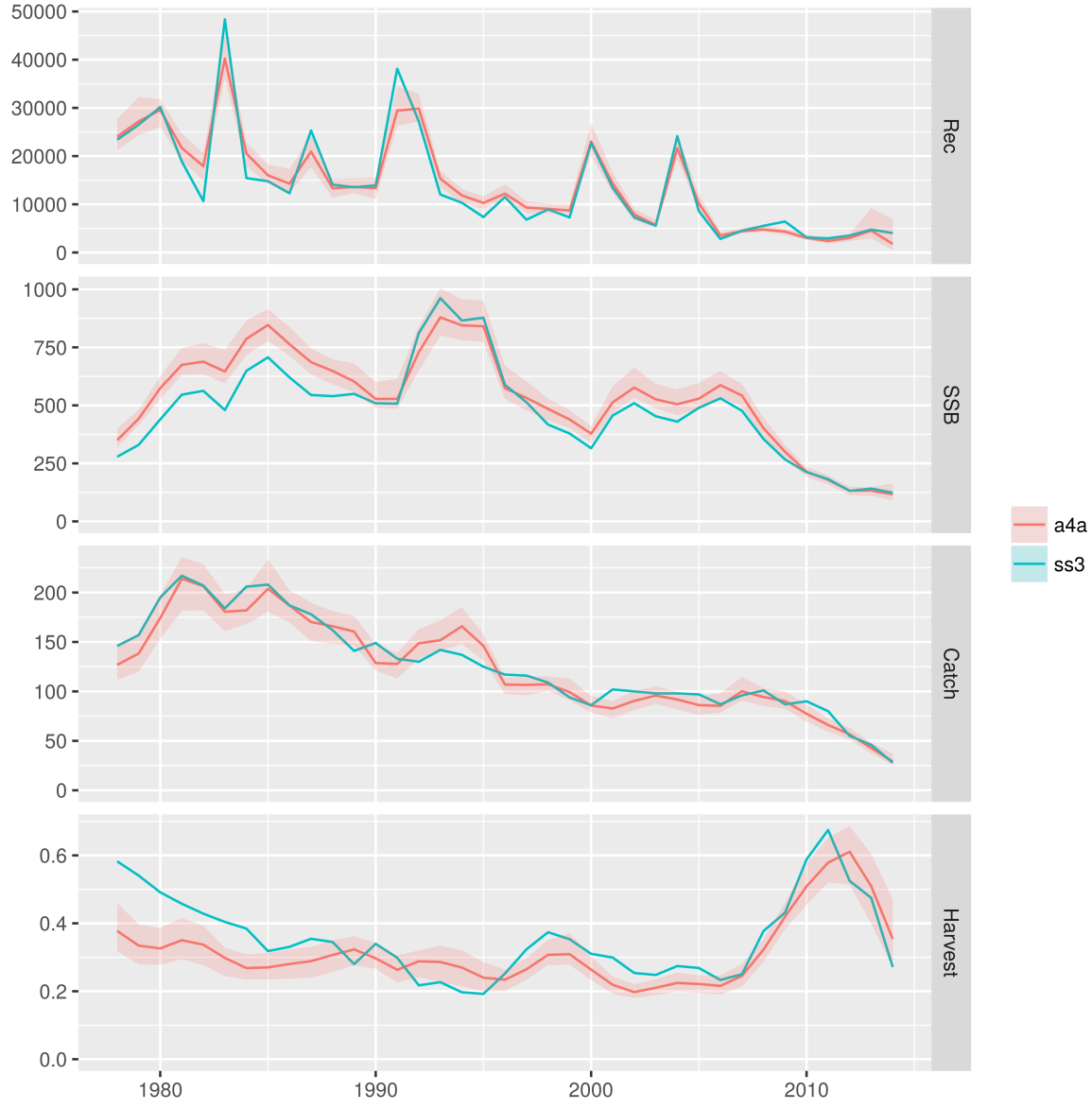

Figure 11: Summary plot

4.2 Bay of Biscay stock

In Divisions VIIIabd sardine is fished mainly by France and Spain. Fisheries in this area are important for both countries, economically and socially. Sardine is used for human consumption, fresh and canned.

The French fishery of sardine is split in two groups defined by the gears used: purse seine and pelagic trawl operated by pair trawlers. The number of vessels has been relatively stable since 1993, with around 30 purse seiners and 20 trawlers. Purse seiners target sardine more or less all year round with a peak in the summer. In average, these vessels are responsible for 80 % of the total annual landings of sardine along the French Atlantic coast. In addition, around 100 Spanish purse seine vessels registered in the Basque Country, Cantabria, Asturias and Galicia are licensed to fish sardine in Division VIIIb (Bureau Veritas, 2010). These vessels fish sardine mainly in spring and autumn.

Sardine is one of the most important species in French fisheries in terms of quantity landed (Figure 2). French landings consistently increased from 1983 to 2008, with values ranging from 4367 tonnes in 1983 to 21104 tonnes in 2008 (Figure 2). Since 2009, they display a decreasing trend which stopped in 2013 with 20 066 tonnes landed, close to the historical series maximum. About 90% of French catches are taken by purse-seiners while the remaining 10% is reported by pelagic trawlers (mainly pair trawlers). The largest catches are taken during the Summer. Almost all the catches are taken in southwest Brittany.

Spanish landings averaged around 4000 tonnes in the late 1990s early 2000s, decreased until 2010 to below 1000 tonnes. Since 2011, landings raised sharply, reaching 16 237 tonnes in 2014. The recent increase is due to fishing restrictions implemented for the Iberian stock.

There is no analytic assessment for this stock. A trend-based assessment is based on a combined standardized index of abundance from two annual surveys: abundance estimates from the PELGAS acoustic survey and egg abundance from the BIOMAN DEPM survey. The PELGAS and BIOMAN surveys are carried out during the Spring since 1999, to estimate the spawning stock biomass. PELGAS provides spawning biomass and abundance at age estimates for the population in the area. The survey based monitoring system provides population estimates by the middle of the year, when a small part of the annual catches have been already taken. The trend based assessment shows an increasing trend of SBB over the last five years (ICES, 2015). There have been several good recruitments in recent years, and the 2015 recruitment is indicated to be the highest of the historical series as indicated by proportion of age 1 individuals observed during the survey.

5. Modeling the spatial dynamics using sub-units/lattices

5.1 Data

The data available to the group consisted in time series of:

- total catch weight,
- catch numbers-at-age,
- mean weight-at-age in the catch
- acoustic survey abundance index in numbers-at-age
- DEPM survey biomass index,
- mean weight-at-age in the stock,
- maturity ogive in proportion of mature individuals at age.

The dataset used in the a4a assessment of the Atlanto-Iberian stock for the whole time series, 1978-2015, was the same used in ICES assessment with SS3 (ICES, 2015). The acoustic survey in the last year (2015) was not used in the a4a assessment.

Datasets for the NW and S stocks were built from data disaggregated by the five ICES sub-divisions used to report to ICES assessment working groups (VIIIc, IXa-North, IXa Central-North, IXa-Central South, IXa South Algarve and IXa-South Cadiz, Figure 5), compiled from 1992 to 2015 reports. Time series of catch data and maturity ogive go from 1991 to 2014. Time series of acoustic and DEPM surveys go from 1996 and 1997, respectively, to 2014. The dataset pooled from the NW and S datasets showed some diferences to the dataset for the Atlantic-Iberian stock used in the ICES stock assessment (ICES, 2015). Although most diferences were small (<5%), there were some major differences (>20%) in catches and acoustic survey numbers at age in some years, which could not be sorted out for the exercise carried out in the meeting.

For the Northern stock input data was restricted to Division VIIIab, as no age structured index is available for the catch data in subarea VII. Because catches at age start in 2002, all input data (catches and surveys) covered the period 2002-2014, borrowing the maturity and mean weights at age data from the input data reported in ICES (2015).

The analysis regarding the scenario of a single stock unit in the entire Areas IX and VIII was therefore restricted to the period 2002-2014 for which input data is available from both Areas.

```
# load
load("../analysis/BB/BBdata.RData")
load("../analysis/IB/IB.Rdata")
load("../analysis/NW/NW.Rdata")
load("../analysis/S/S.RData")

# Set plusgroup for BoB sardine
BB.stkpg <- setPlusGroup(BB.stk, 6)

# Trimming
yearsel = 2002:2014
BB.temp <- trim(BB.stkpg, year = yearsel)
IB.temp <- trim(IB.stk, year = yearsel)
NW.temp <- trim(NW.stk, year = yearsel)
S.temp <- trim(S.stk, year = yearsel)
```

The objects for the overall stock, required to run the stock assessment models, had to be created by combining the disaggregated data.

```
# stock
A.stk <- FLStock()
name(A.stk) <- "ALL REGIONS ATLANTO-IBERIAN SARDINE"
desc(A.stk) <- "prepared for a4a workshop - 15/12/2015"
A.stk@range <- IB.temp@range
A.stk@m.spwn <- IB.temp@m.spwn
A.stk@harvest.spwn <- IB.temp@harvest.spwn
A.stk@harvest <- BB.temp@harvest
A.stk@mat <- S.temp@mat
A.stk@m <- S.temp@m
A.stk@discards <- BB.temp@discards
A.stk@discards.wt <- BB.temp@discards.wt
A.stk@discards.n <- BB.temp@discards.n
A.stk@landings <- BB.temp@landings + S.temp@landings * 1000 +
    NW.temp@landings * 1000
units(A.stk@landings) <- "tons"
A.stk@landings.n <- BB.temp@landings.n + S.temp@landings.n *
    1000 + NW.temp@landings.n * 1000
units(A.stk@landings.n) <- "thousands"
A.stk@catch <- A.stk@landings
A.stk@catch.n <- A.stk@landings.n
A.stk@landings.wt <- (BB.temp@catch.wt * BB.temp@landings.n +
    NW.temp@catch.wt * NW.temp@landings.n * 1000 + S.temp@catch.wt *
    S.temp@landings.n * 1000)/A.stk@landings.n
units(A.stk@landings.wt) <- "kg"
A.stk@catch.wt <- A.stk@landings.wt
A.stk@stock <- S.temp@stock
A.stk@stock.n <- S.temp@stock.n
A.stk@stock.wt <- (BB.temp@stock.wt * BB.temp@landings.n + NW.temp@stock.wt *
    NW.temp@landings.n * 1000 + S.temp@stock.wt * S.temp@landings.n *
    1000)/A.stk@landings.n
units(A.stk@stock.wt) <- "kg"
```

The survey indices required processing before being merged, which raised some issues regarding the methods used. For both acoustic and DEPM indices, when data were missing (for example because the survey was triennal or technical issues prevented the survey to take place for a given year), the missing values were simply interpolated. The acoustic index was computed as the sum of all acoustic indices for each area. The DEPM survey in the south and the egg count in the Bay of Biscay were kept separately. A simulation was done considering a single overall acoustic time series and another one was carried out with all acoustic surveys taken separately.

```
BB1 <- trim(BB.idx[[1]], year = yearsel, age = 1:6)
BB2 <- trim(BB.idx[[2]], year = yearsel, age = 1:6)
IB1 <- trim(IB.idx[[1]], year = yearsel, age = 1:6)
IB2 <- trim(IB.idx[[2]], year = yearsel, age = 1:6)
NW1 <- trim(NW.idx[[1]], year = yearsel, age = 1:6)
NW2 <- trim(NW.idx[[2]], year = yearsel, age = 1:6)
S1 <- trim(S.idx[[1]], year = yearsel, age = 1:6)
S2 <- trim(S.idx[[2]], year = yearsel, age = 1:6)
desc(BB2) <- "BB Egg"
desc(BB1) <- "BB Acoustic"
desc(IB1) <- "IB Acoustic"
desc(IB2) <- "IB DEPM"
desc(NW1) <- "NW Acoustic"
desc(NW2) <- "NW DEPM"
desc(S1) <- "S Acoustic"
desc(S2) <- "S DEPM"
name(BB2) <- "BB Egg"
name(BB1) <- "BB Acoustic"
name(IB1) <- "IB Acoustic"
name(IB2) <- "IB DEPM"
```

```
name(NW1) <- "NW ACoustic"
name(NW2) <- "NW DEPM"
name(S1) <- "S Acoustic"
name(S2) <- "S DEPM"

# Separate object file => NEEDS MORE EXPLANATION
NW1@index[, 3] <- (NW1@index[, 2] + NW1@index[, 4])/2
NW1@index[, 11] <- (NW1@index[, 10] + NW1@index[, 12])/2
S1@index[, 3] <- (S1@index[, 2] + S1@index[, 4])/2
S1@index[, 11] <- (S1@index[, 10] + S1@index[, 12])/2

# AC: Aggregated acoustic index
AC <- NW1
name(AC) <- "Aggr Acoustic"
desc(AC) <- "Aggr Acoustic"
AC@index <- BB1@index + NW1@index * 1000 + S1@index * 1000
AC@range <- BB1@range
units(AC@index) <- "Thousands"
A.idx <- FLIndices(AC, BB2, NW2, S2)

# DP: Aggregated DEPM index
DP <- NW2
name(DP) <- "Aggr DEPM"
desc(DP) <- "Aggr DEPM"
DP@index <- NW2@index * 1000 + S2@index * 1000
DP@range <- NW2@range
units(DP@index) <- "Thousands"
DP@index[, 2] <- (DP@index[, 1] * 2 + DP@index[, 4] * 1)/3

# indices objects
A.idx <- FLIndices(AC, BB2, DP)  # Aggr Acoustic + DEPM
A.idx2s <- FLIndices(BB1, NW1, S1, DP)  # Aggr DEPM but separate acoustic
```

5.2 Methods

Based on initial discussions it was decided to start by focusing on fishing mortality models, to explore the options available in the a4a stock assessment model. After agreeing on the fishing mortality model structure, the analysis was focused on the catchability models. These processes were looped until a final setting was achieved.

To carry out the comparison across sub-units the models used were kept as similar as possible, to mitigate the effect that the choice of model can have on the final results.

The group decided to keep a set of different models for each sub-unit, each using distinct survey settings, as follows:

- f model - bivariate tensor with (in some cases) smooth on age to decrease the number of degrees of freedom;
- q models
  - q1: smooth catchability across ages and years (qmod <- list(~ s(age, k=5), ~ 1)),
  - q2: constant catchability across ages and years (qmod <- list(~ 1, ~ 1)),
  - q3: smooth catchability across ages and years with extra weight for survey (qmod <- list(~ s(age, k=5), ~ 1); index.var(idx) <- 0.5),
  - q4: constant catchability across ages and years with extra weight for survey (qmod <- list(~ 1, ~ 1); index.var(idx) <- 0.5),
  - q5: constant catchability across ages and years without the depm survey (qmod <- list(~ 1)).

Uncertainty was estimated using MCMC with the ADMB implementation, which, in the most recent version, can be assessed through the FLa4a package.

In the case of the overall stock, a sensitivity analysis about survey's data processing options was carried out, to investigate the robustness of the assessment results.

The following naming convention was used, to facilitate sharing R objects among the participants:

- prefix for stocks
  - S: south
  - BB: Bay of Biscay
  - NW: Northwest
  - A: All
  - IB: Iberian
- for q options
  - q1: smooth catchability across ages and years
  - q2: constant catchability across ages and years
  - q3: smooth catchability across ages and years with extra weight for survey
  - q4: constant catchability across ages and years with extra weight for survey
  - q5: constant catchability across ages and years without the depm survey
- for object types
  - f: likelihood fit
  - r: residuals of the likelihood fit
  - s: stk object with likelihood estimates
  - mc: MCMC fit
  - mcmc: coda object of MCMC fit
  - smc: stk object with MCMC estimates

5.3 The overall stock

The assessment options tested on the overall stock were slightly different from the ones used for the sub-units to account for some specific features of the surveys, which had to be re-processed to merge different time series. To evaluate the impact of those decisions a sensitivity analysis was performed.

5.3.1 q option 1: smoother, no overweighting of survey

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 7))
qmod <- list(~s(age, k = 4), ~1, ~1)
A.q1f <- a4aSCA(A.stk, A.idx, fmodel = fmod, qmodel = qmod)
A.q1r <- residuals(A.q1f, A.stk, A.idx)
A.q1s <- A.stk + simulate(A.q1f, 500)
A.q1mc <- a4aSCA(A.stk, A.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
A.q1mcmc <- as.mcmc(A.q1mc)
A.q1smc <- A.stk + A.q1mc
```

```
plot(A.q1r)
```

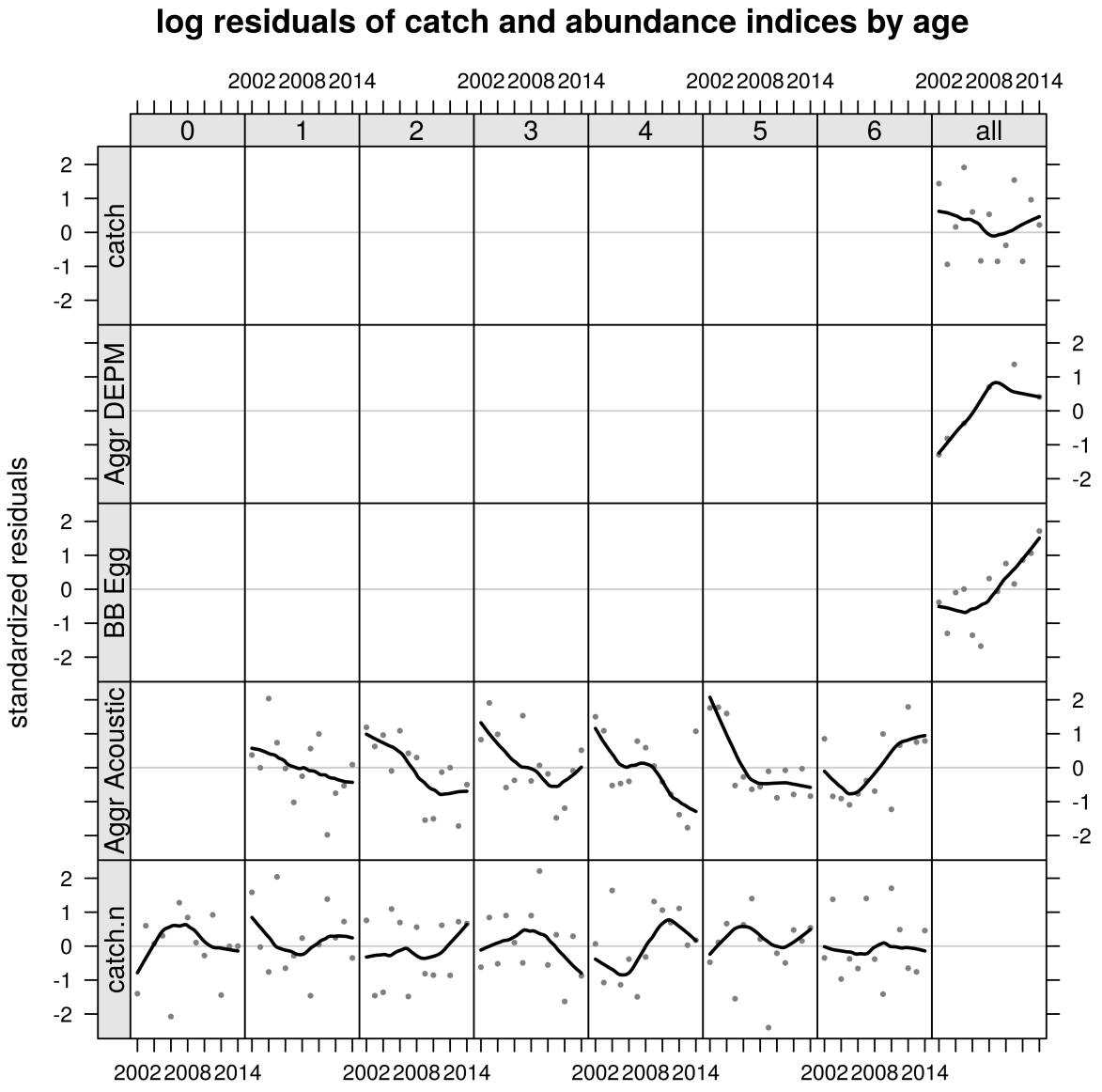

Figure 12: Residuals

```
plot(A.q1f, A.stk)
```

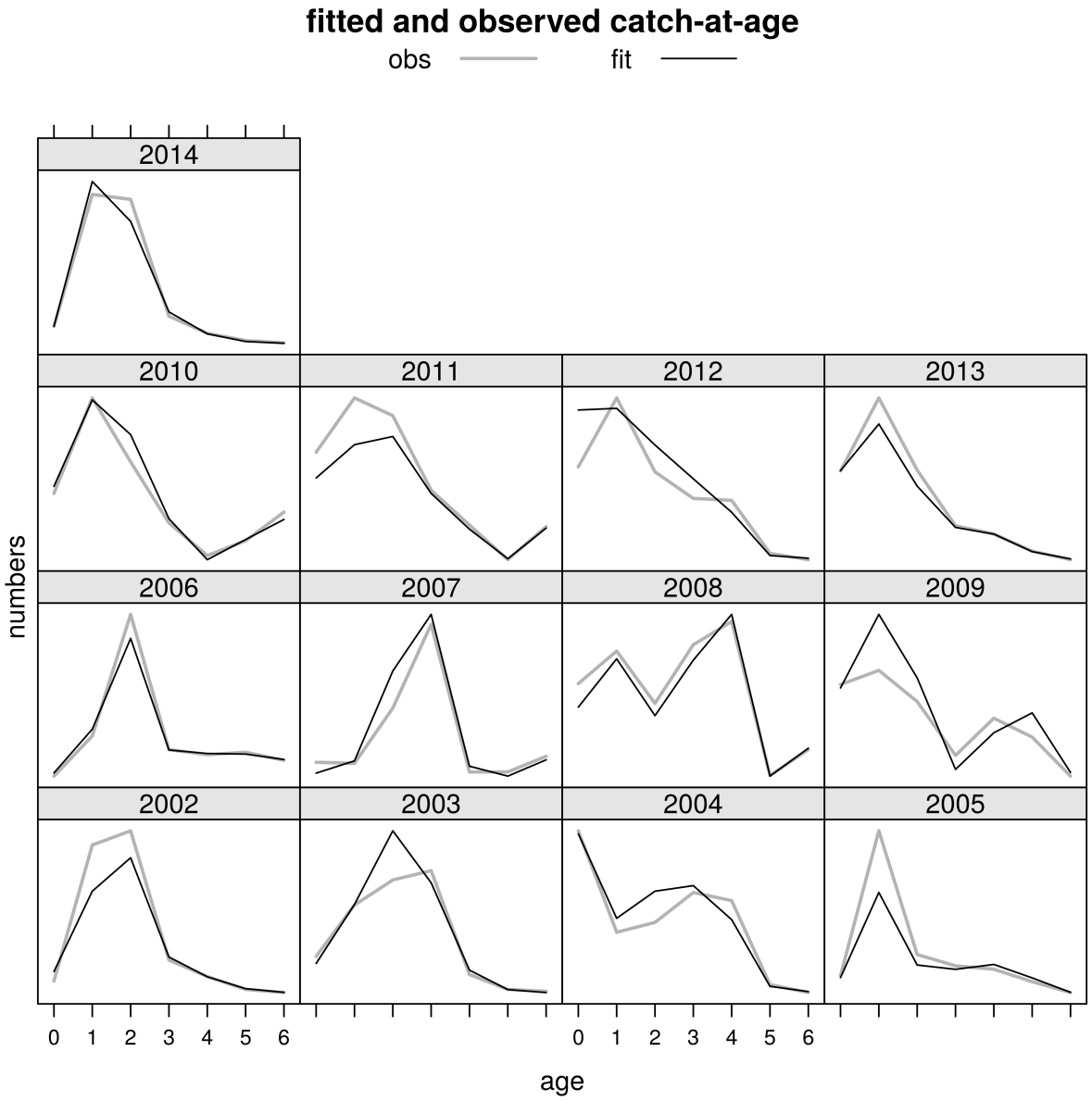

Figure 13: Catch-at-age predictions and observations

```
plot(A.q1f, A.idx[1])
```

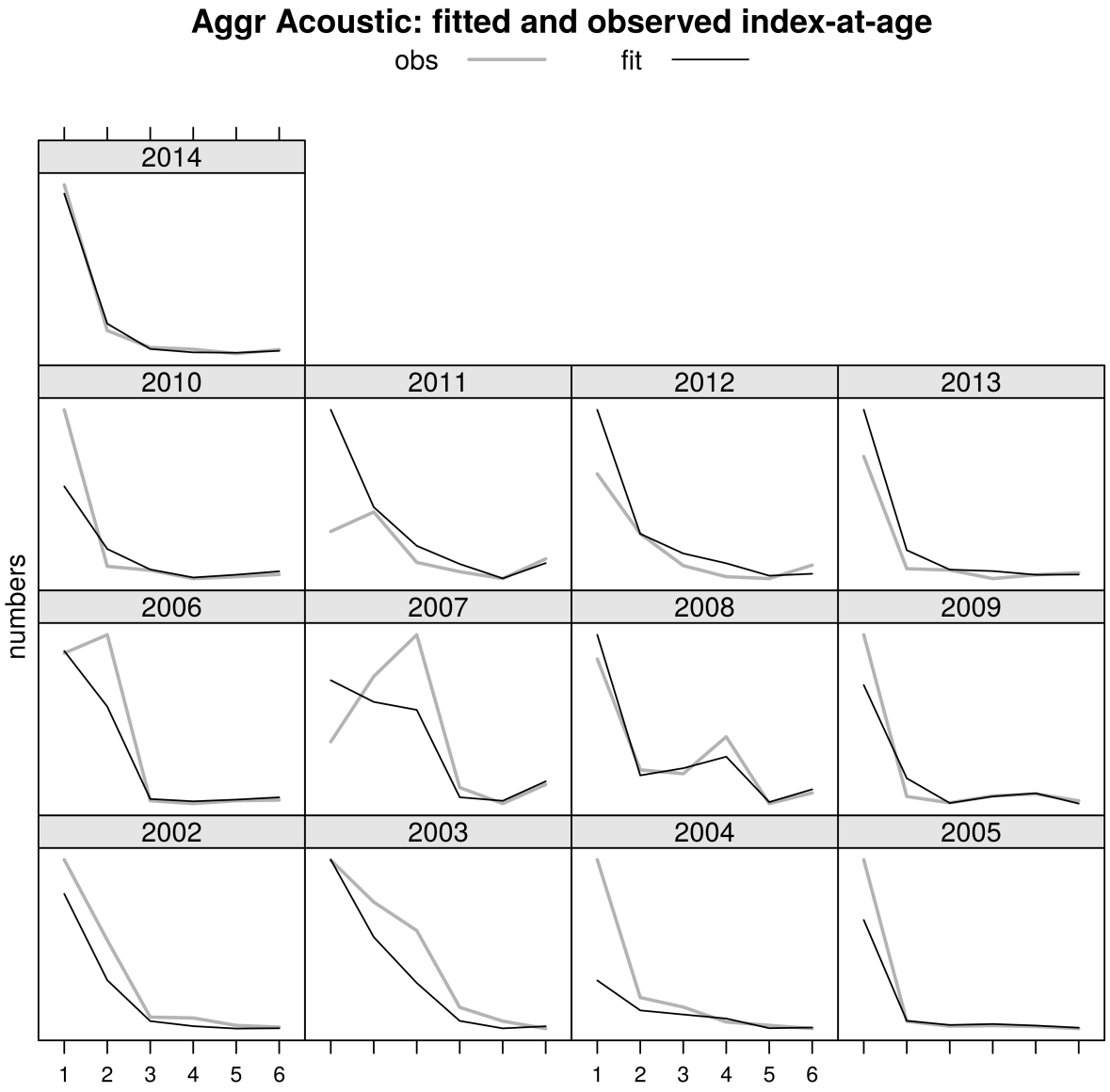

Figure 14: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(A.q1f))
```

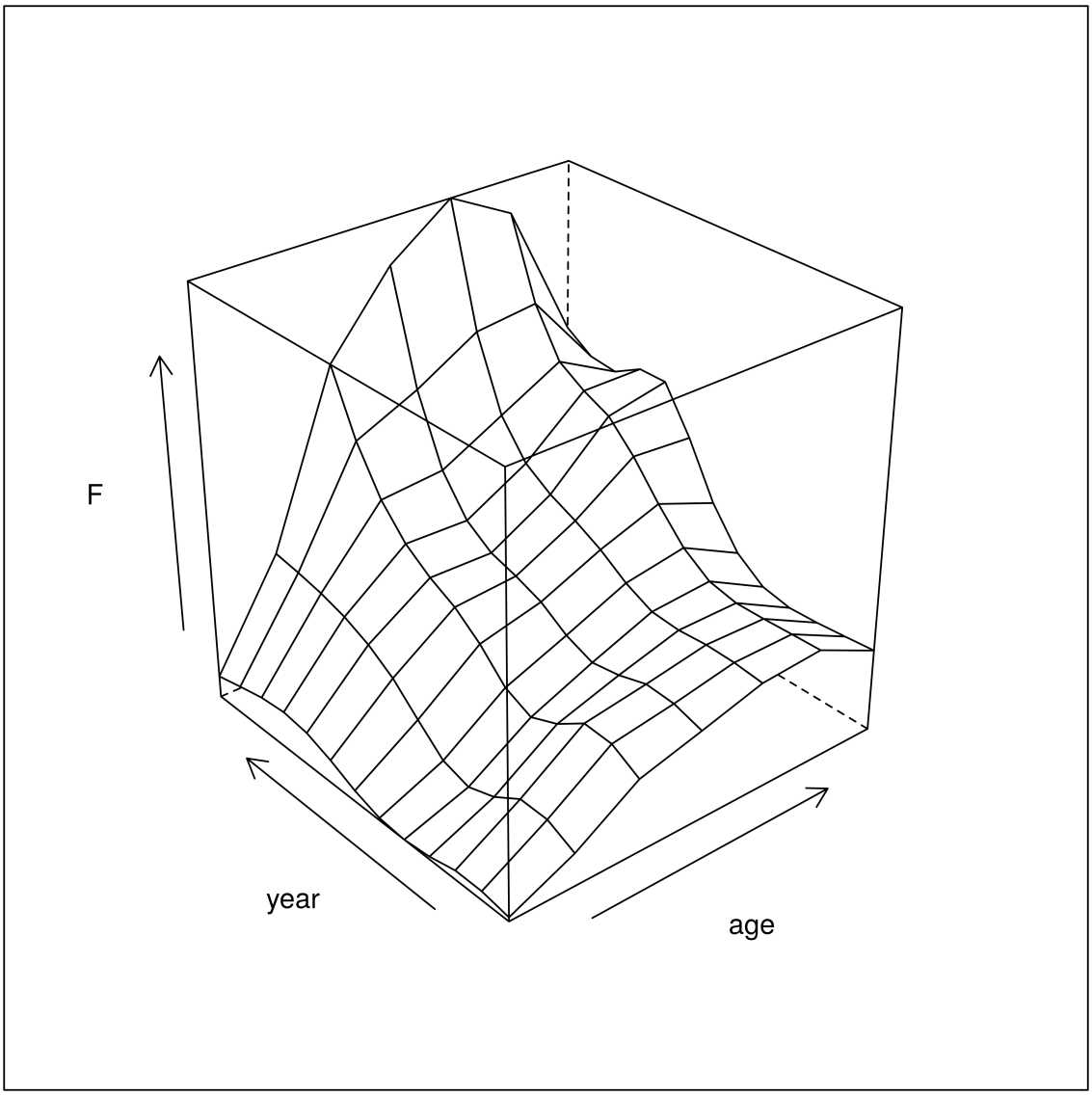

Figure 15: F-at-age estimate

```
plot(A.q1mc)
```

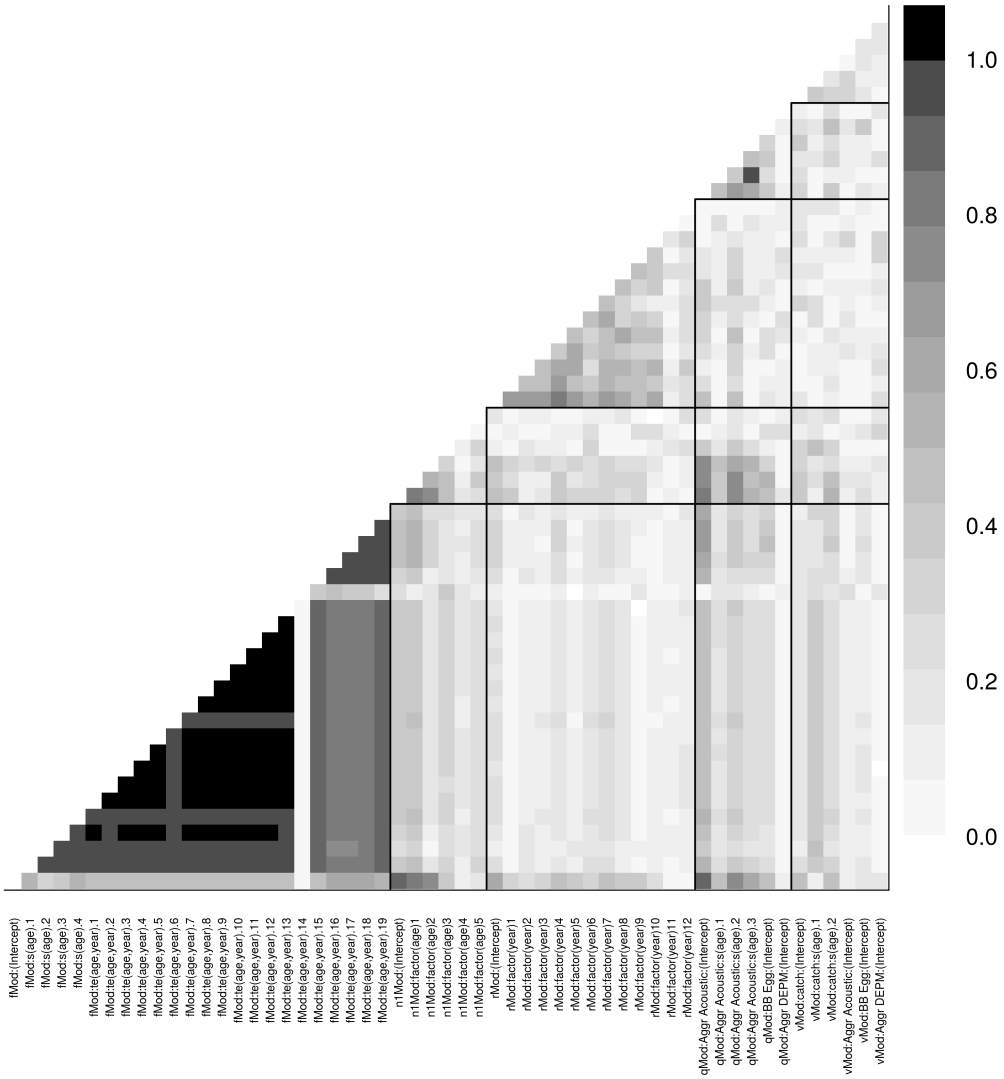

Figure 16: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(A.q1smc)
```

Figure 17: Summary plot

5.3.2 q option 2: constant (at age), no overweighting of survey

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 7))
qmod <- list(~factor(replace(age, age > 1, 2)), ~year, ~1)
A.q2f <- a4aSCA(A.stk, A.idx, fmodel = fmod, qmodel = qmod)
A.q2r <- residuals(A.q2f, A.stk, A.idx)
A.q2s <- A.stk + simulate(A.q2f, 500)
A.q2mc <- a4aSCA(A.stk, A.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
A.q2mcmc <- as.mcmc(A.q2mc)
A.q2smc <- A.stk + A.q2mc
```

```
plot(A.q2r)
```

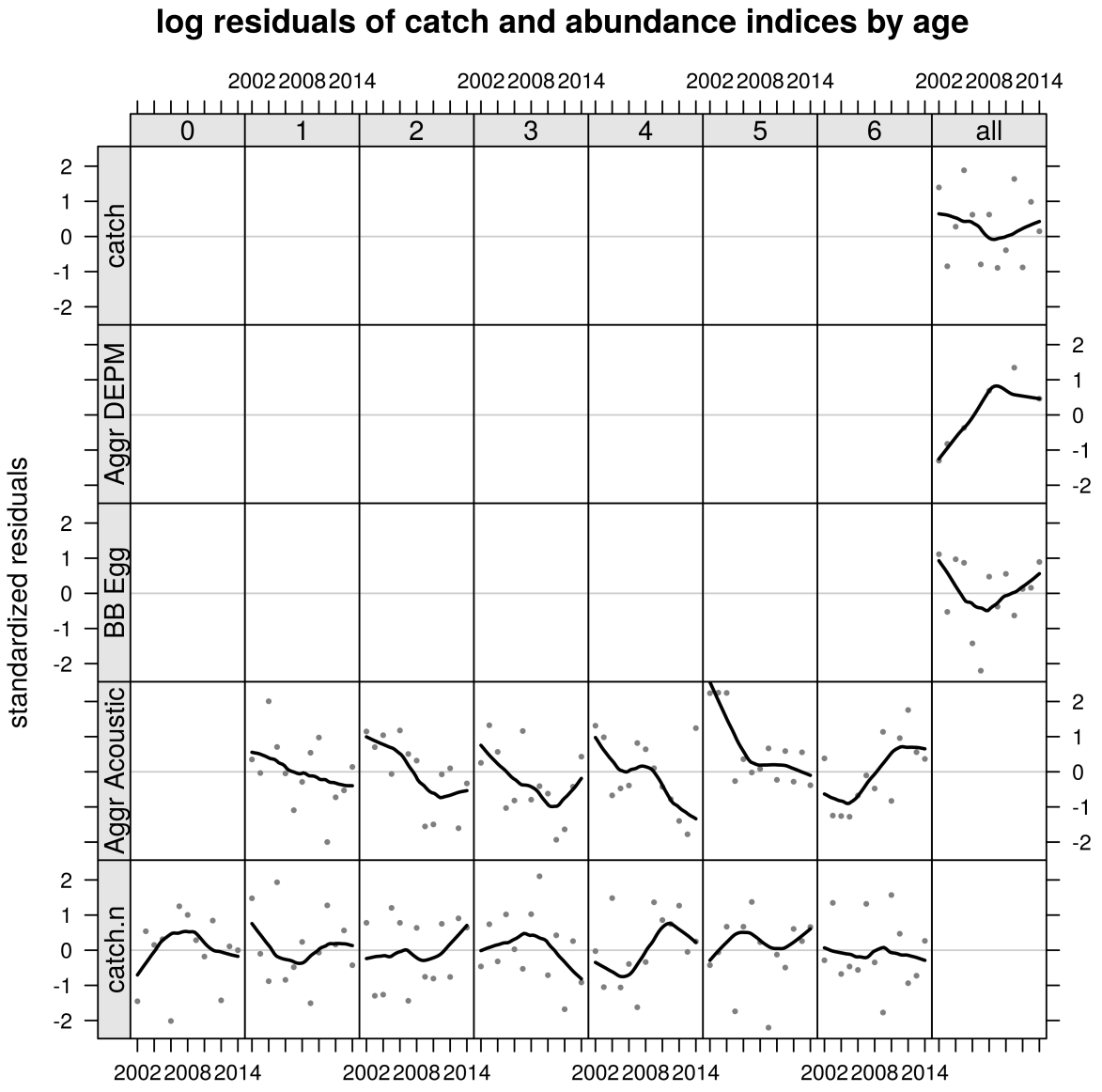

Figure 18: Residuals

```
plot(A.q2f, A.stk)
```

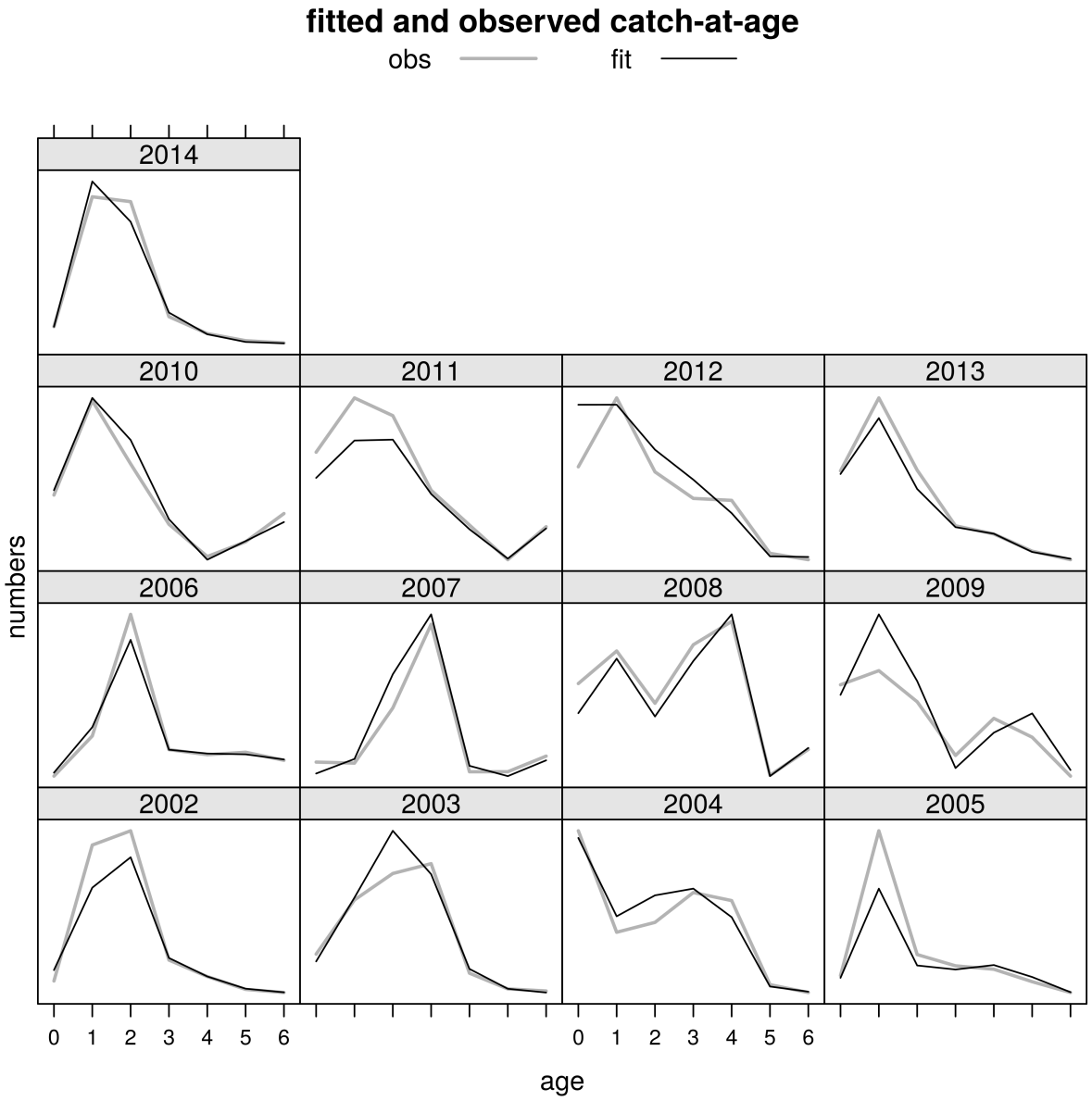

Figure 19: Catch-at-age predictions and observations

```
plot(A.q2f, A.idx[1])
```

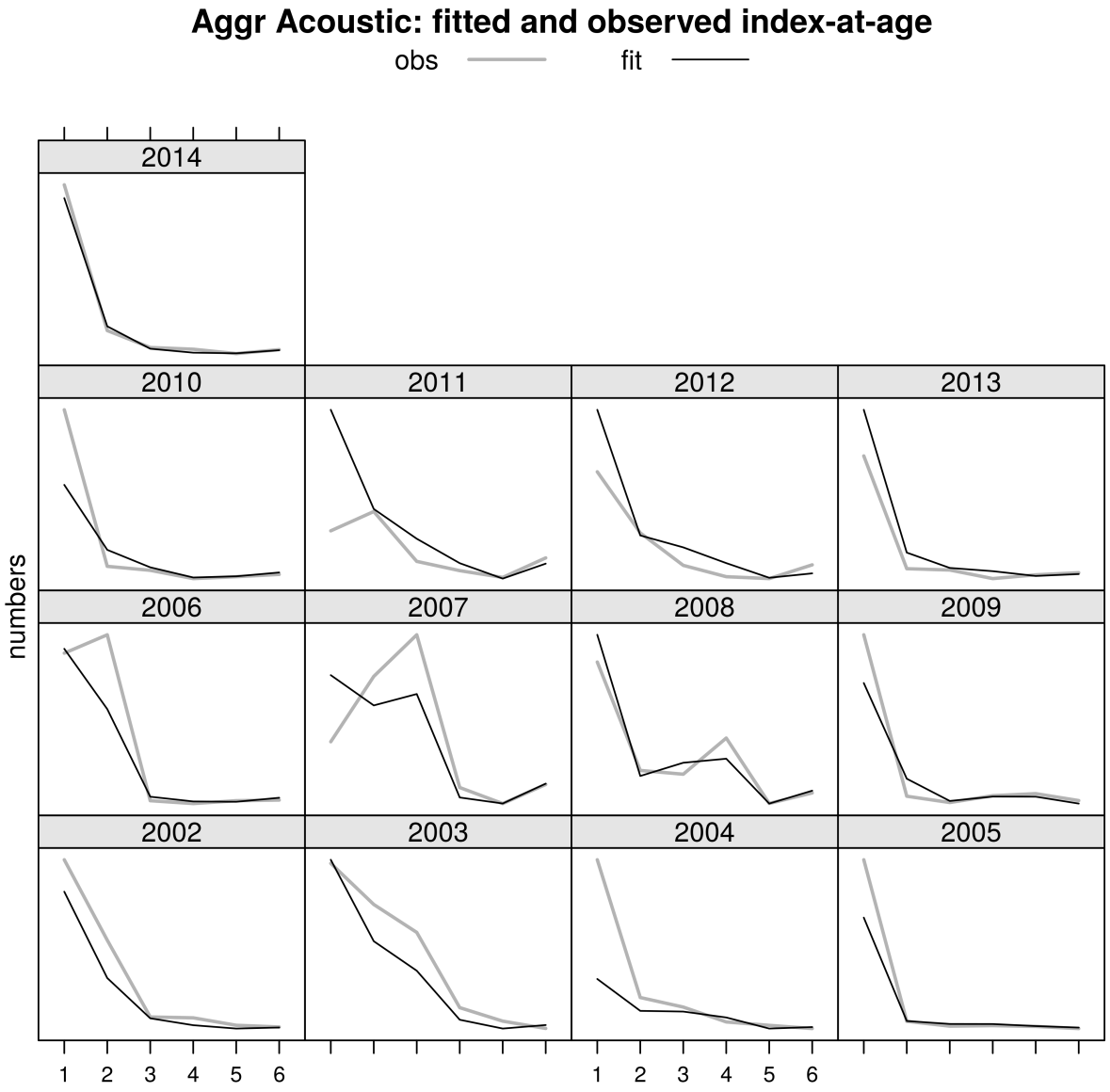

Figure 20: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(A.q2f))
```

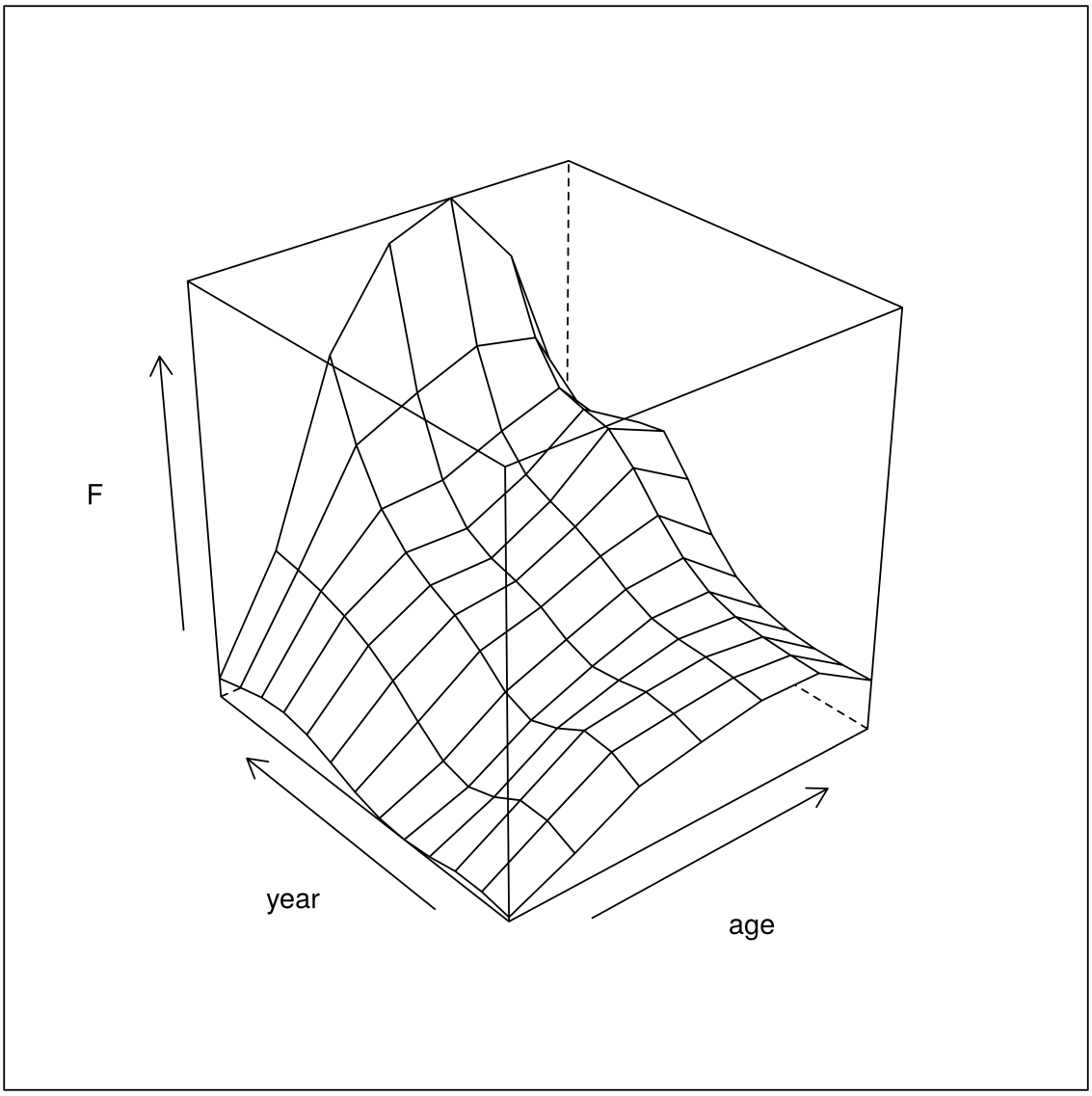

Figure 21: F-at-age estimate

```
plot(A.q2mc)
```

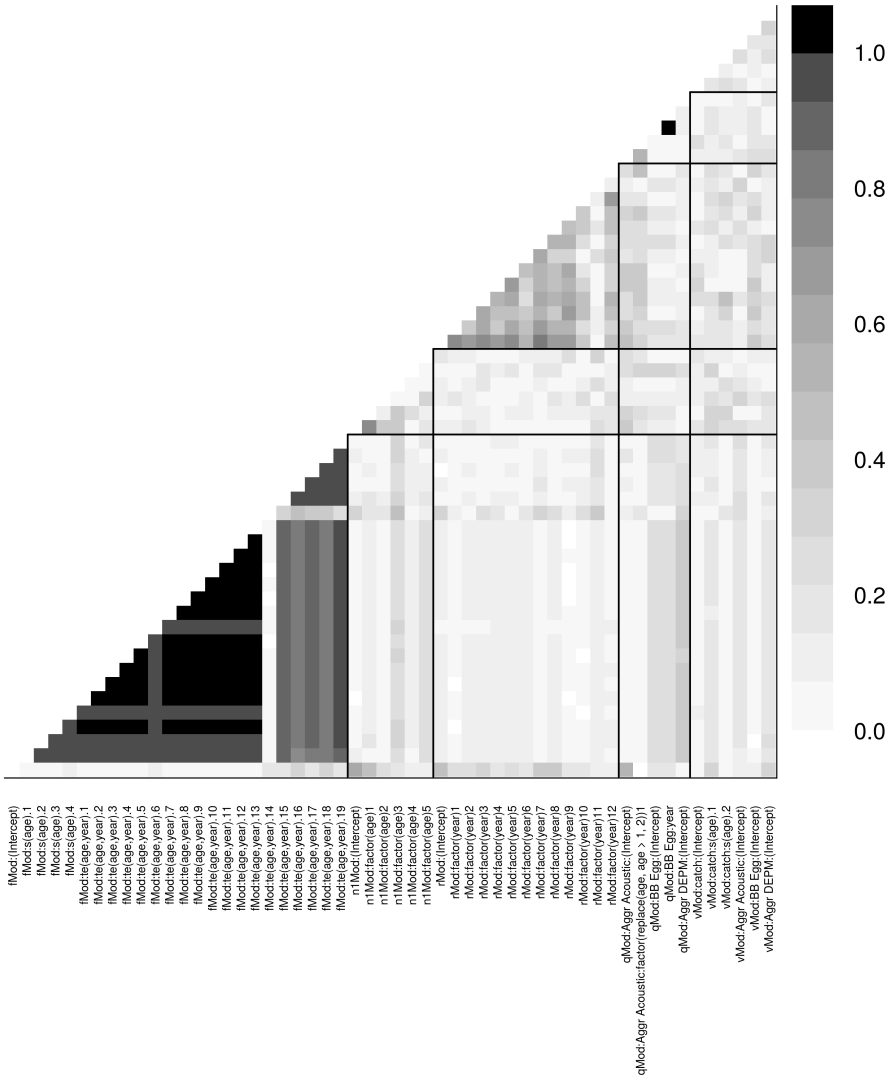

Figure 22: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(A.q2smc)
```

Figure 23: Summary plot

5.3.3 q option 3: smoother, survey overweighting

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 7))
qmod <- list(~s(age, k = 4), ~1, ~1)
A.idx2 <- A.idx
index.var(A.idx2[[1]]) <- 0.5
A.q3f <- a4aSCA(A.stk, A.idx2, fmodel = fmod, qmodel = qmod)
A.q3r <- residuals(A.q3f, A.stk, A.idx2)
A.q3s <- A.stk + simulate(A.q3f, 500)
A.q3mc <- a4aSCA(A.stk, A.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
A.q3mcmc <- as.mcmc(A.q3mc)
A.q3smc <- A.stk + A.q3mc
```

```
plot(A.q3r)
```

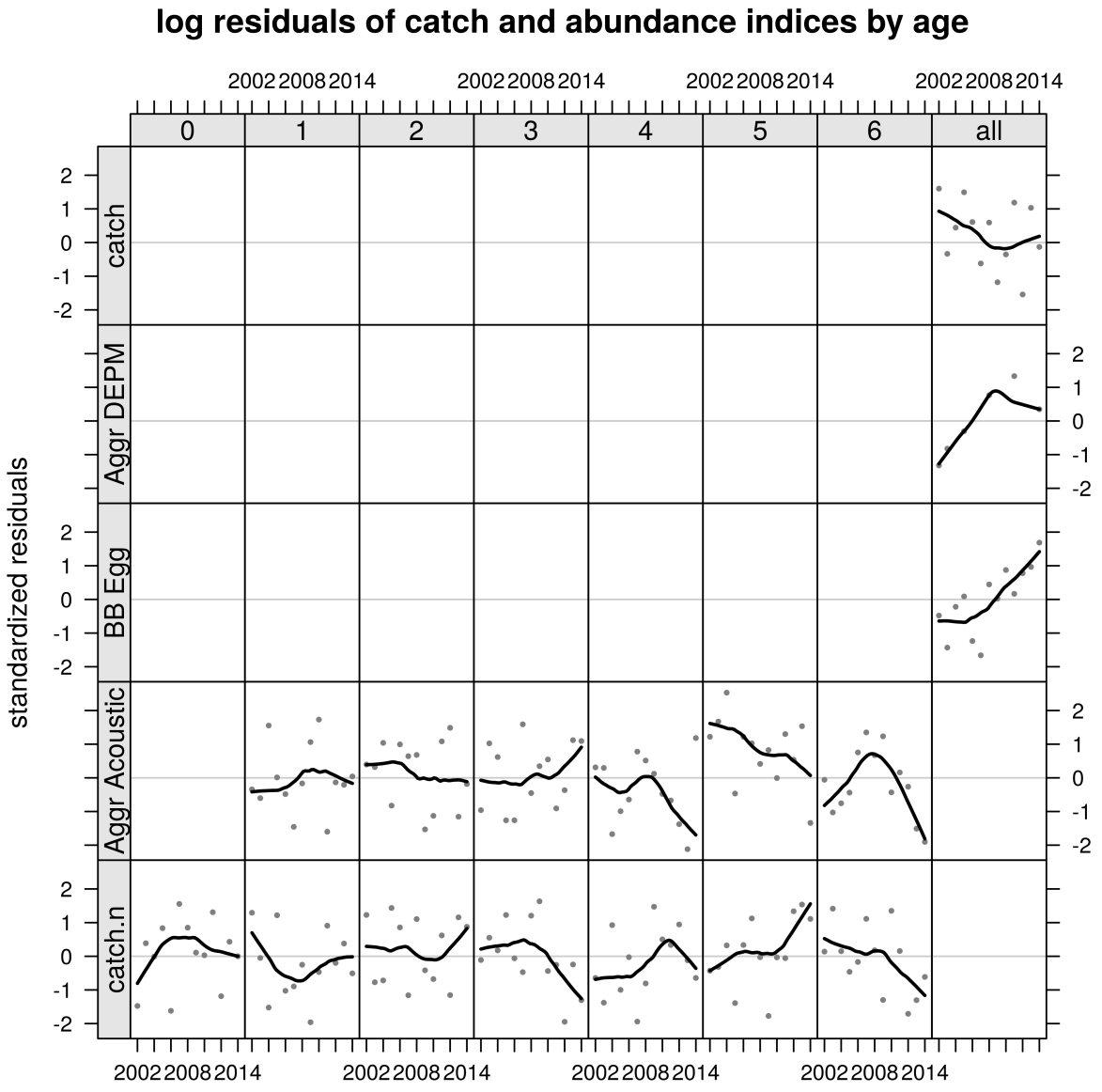

Figure 24: Residuals

```
plot(A.q3f, A.stk)
```

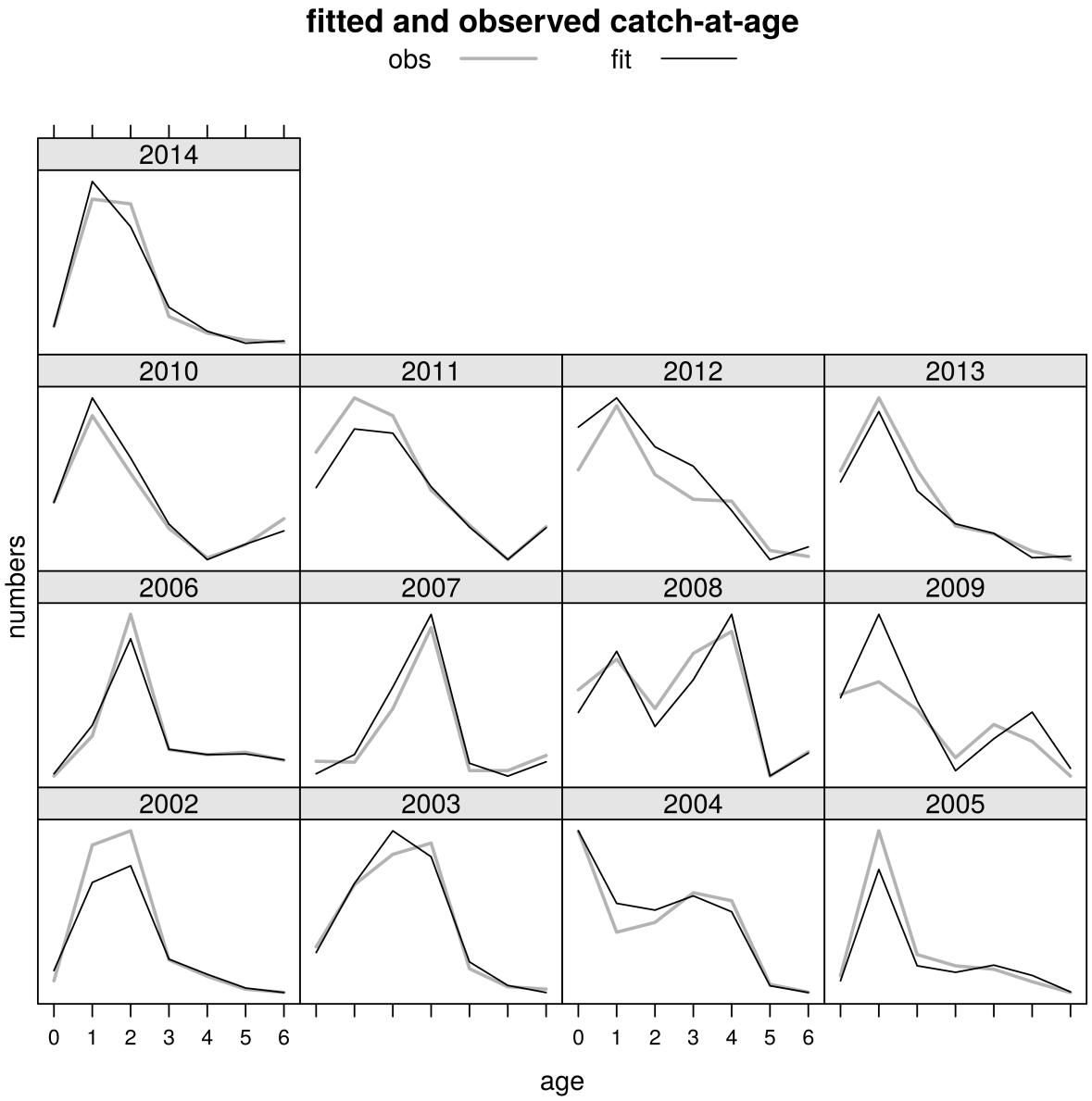

Figure 25: Catch-at-age predictions and observations

```
plot(A.q3f, A.idx2[1])
```

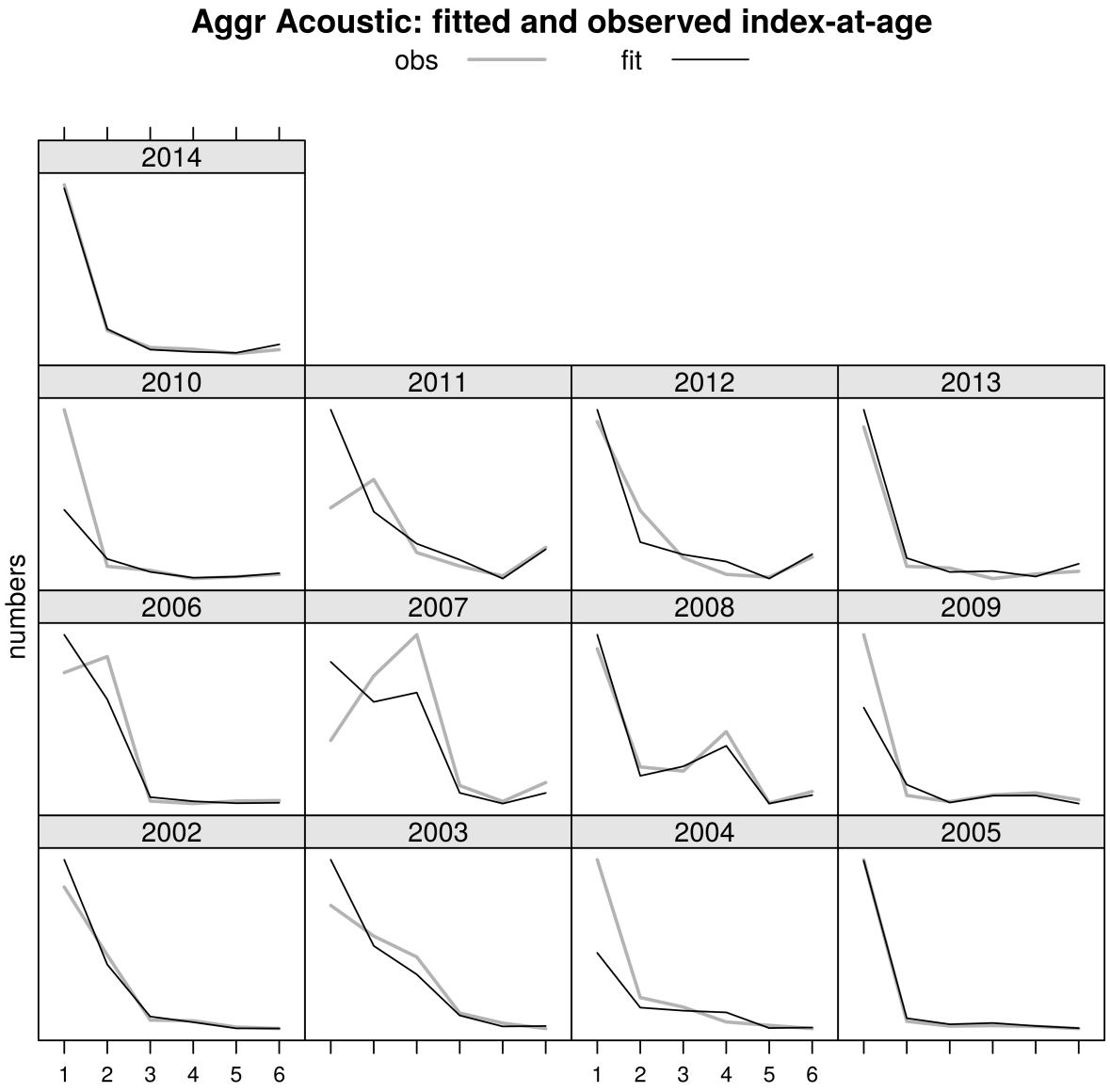

Figure 26: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(A.q3f))
```

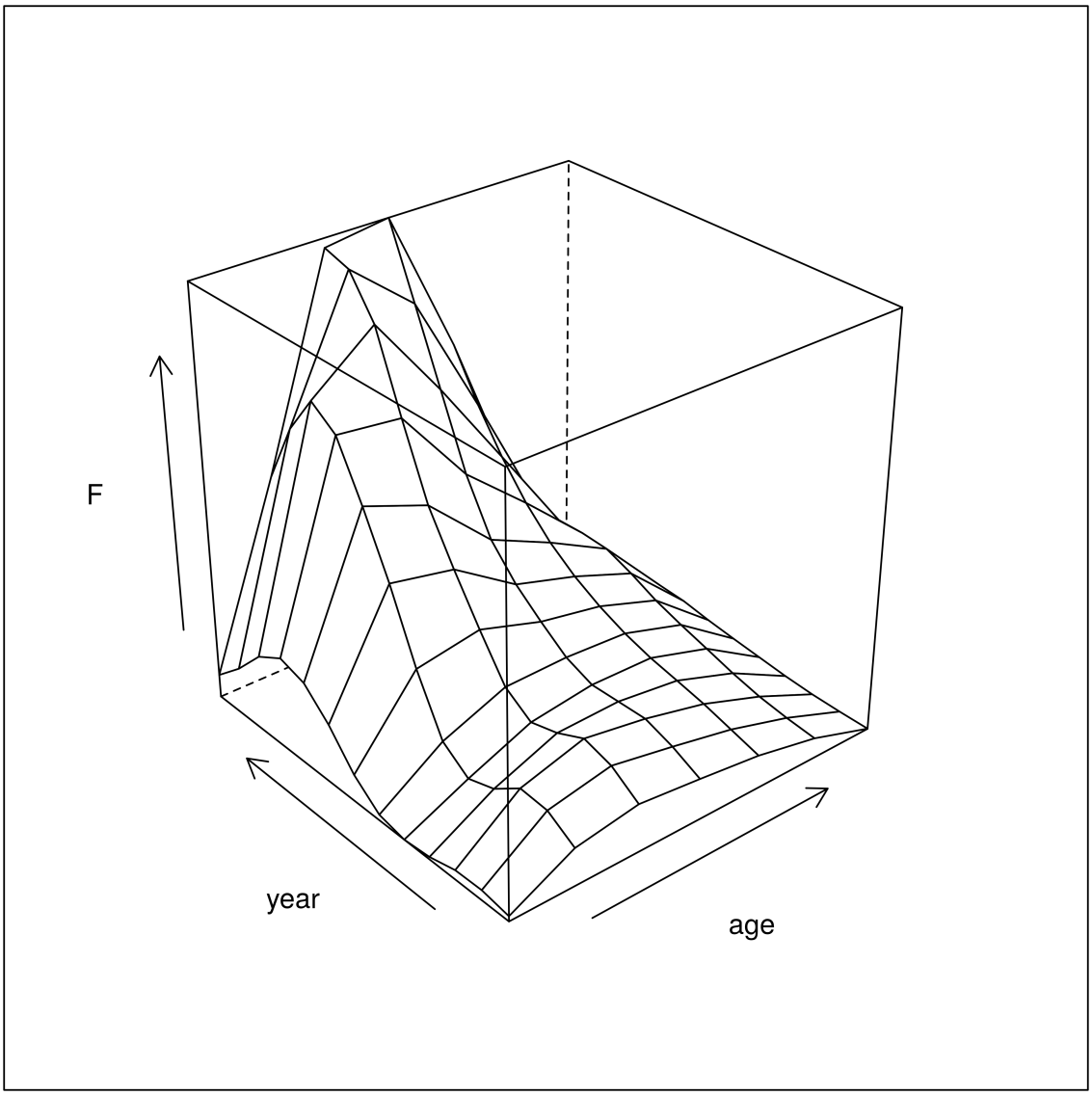

Figure 27: F-at-age estimate

```
plot(A.q3mc)
```

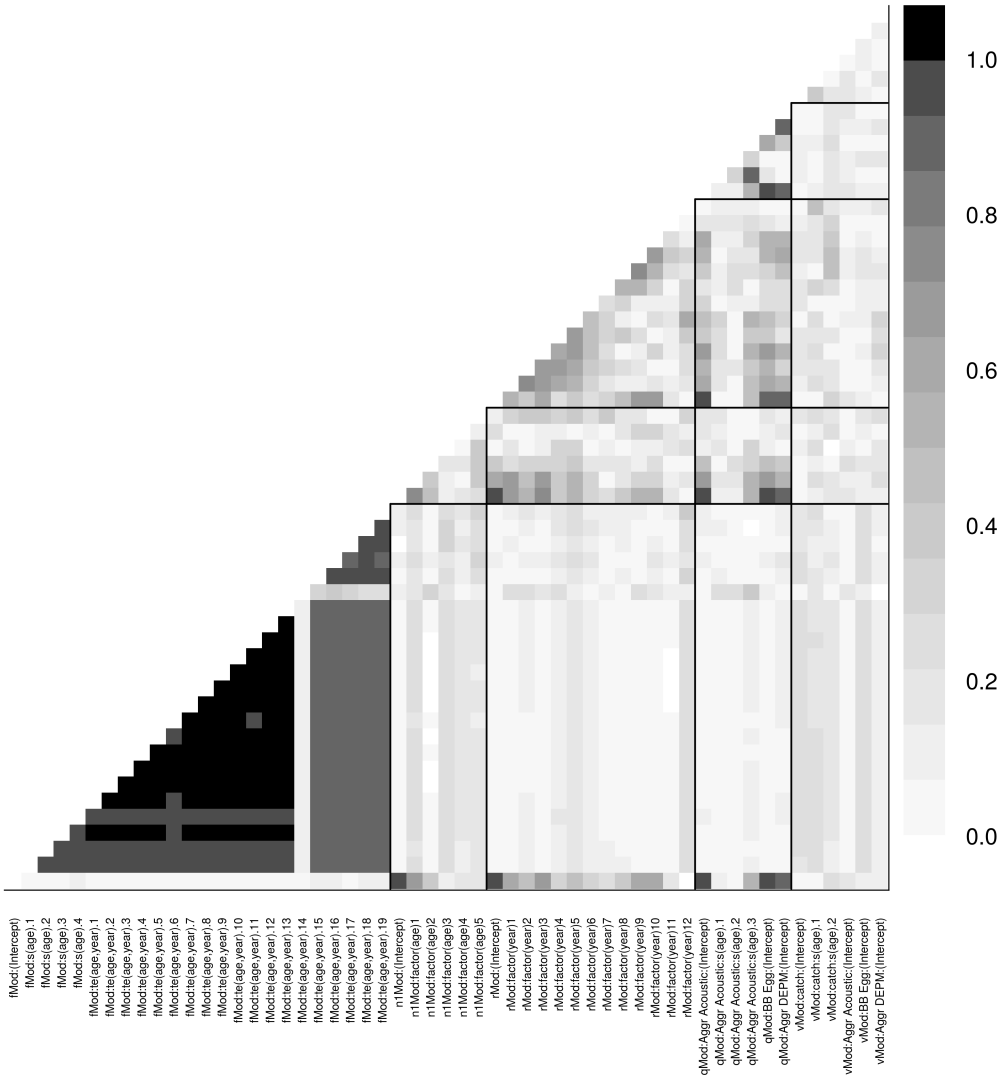

Figure 28: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(A.q3smc)
```

Figure 29: Summary plot

5.3.4 q option 4: constant, survey overweighting

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 7))
qmod <- list(~factor(replace(age, age > 1, 2)), ~year, ~1)
A.idx2 <- A.idx
index.var(A.idx2[[1]]) <- 0.5
A.q4f <- a4aSCA(A.stk, A.idx2, fmodel = fmod, qmodel = qmod)
A.q4r <- residuals(A.q4f, A.stk, A.idx2)
A.q4s <- A.stk + simulate(A.q4f, 500)
A.q4mc <- a4aSCA(A.stk, A.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
A.q4mcmc <- as.mcmc(A.q4mc)
A.q4smc <- A.stk + A.q4mc
```

```
plot(A.q4r)
```

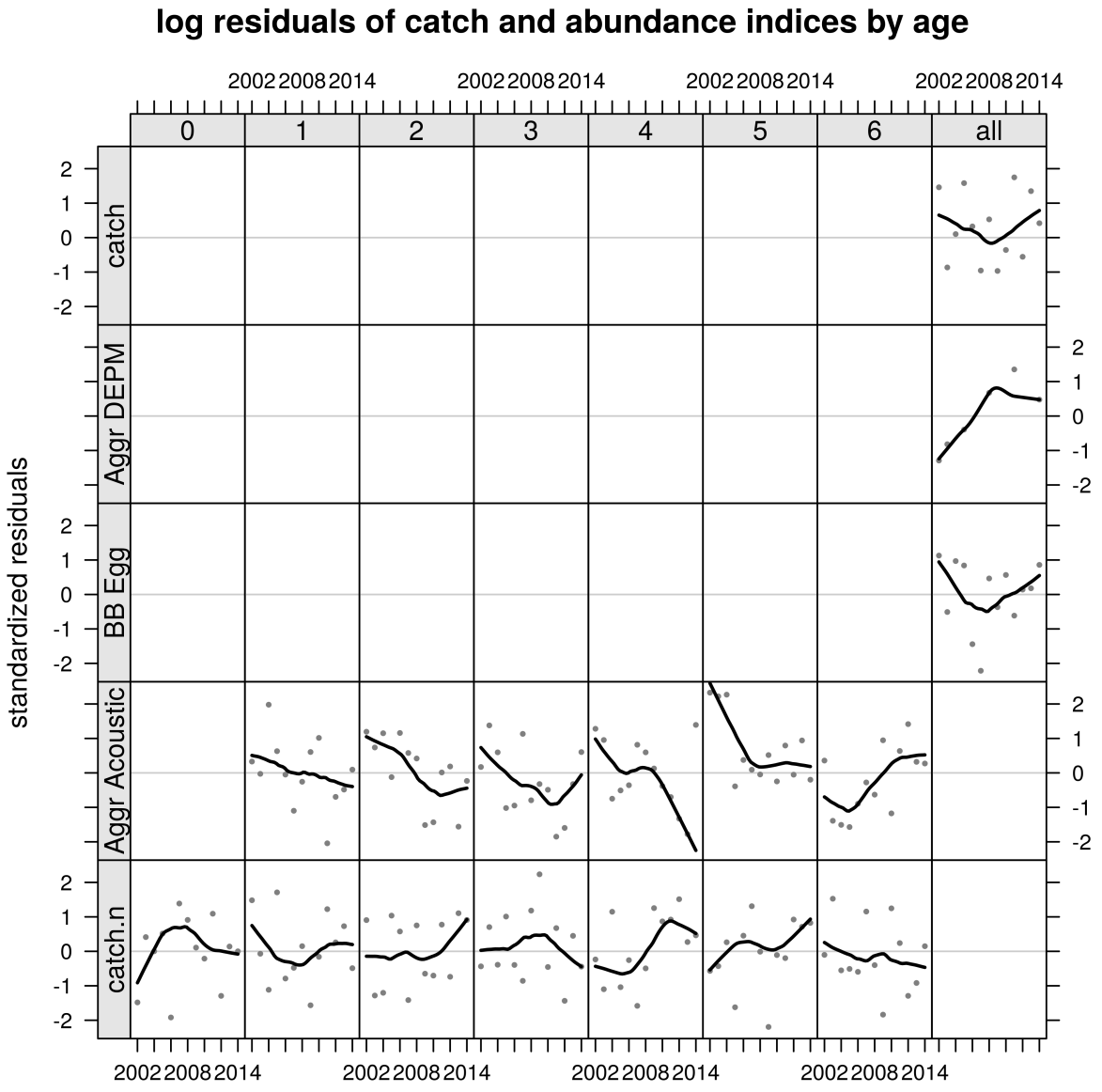

Figure 30: Residuals

```
plot(A.q4f, A.stk)
```

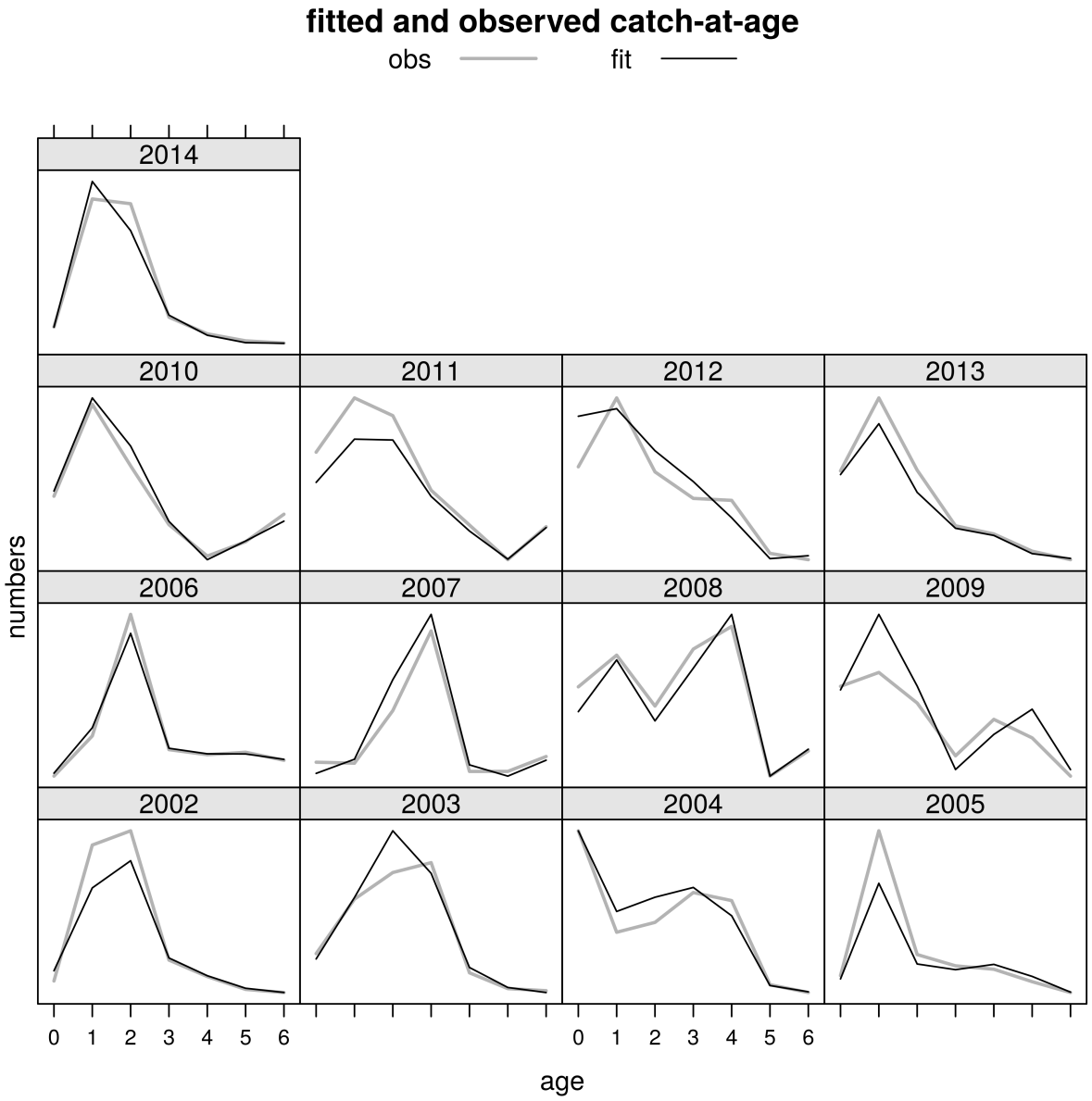

Figure 31: Catch-at-age predictions and observations

```
plot(A.q4f, A.idx2[1])
```

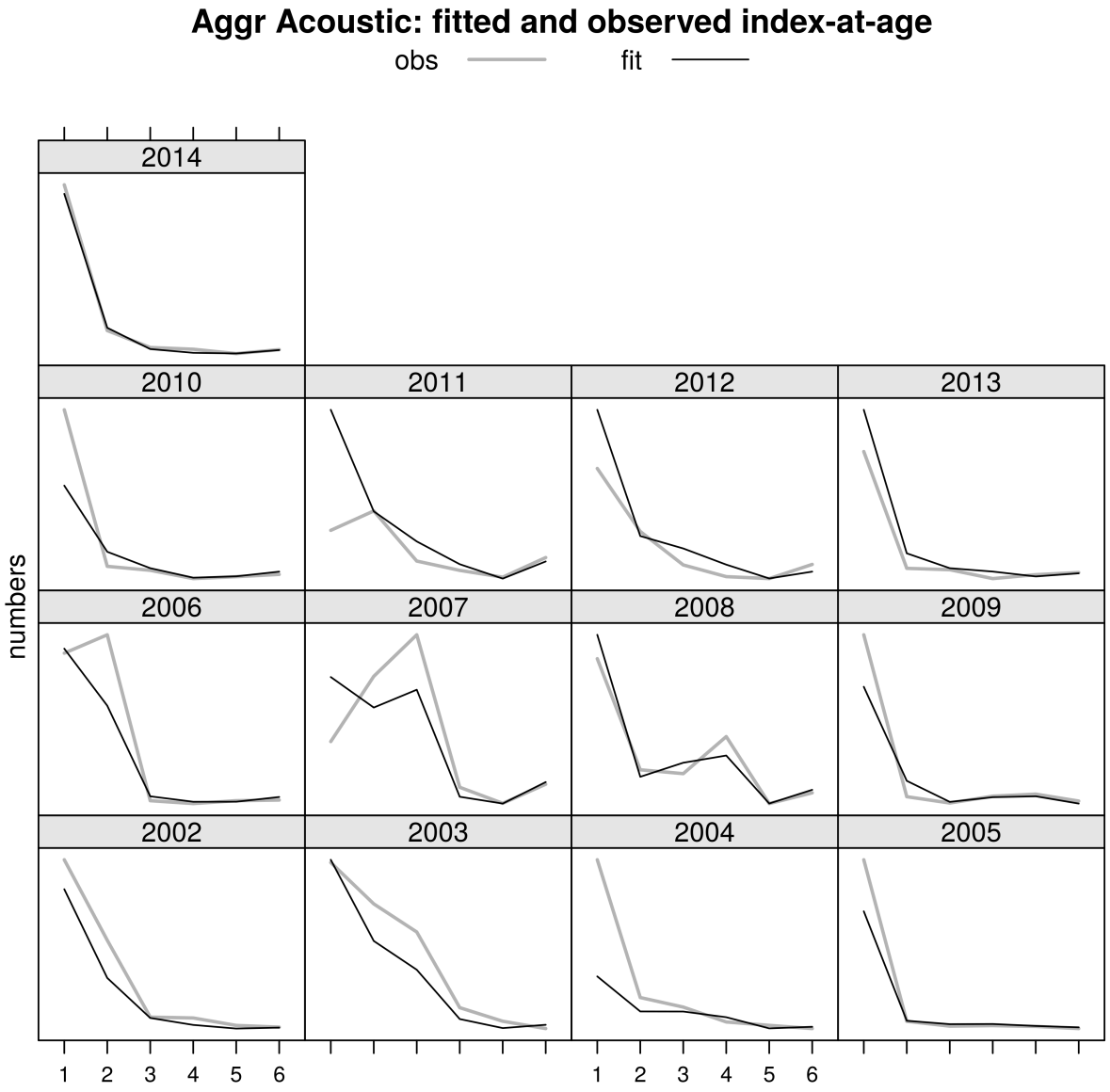

Figure 32: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(A.q4f))
```

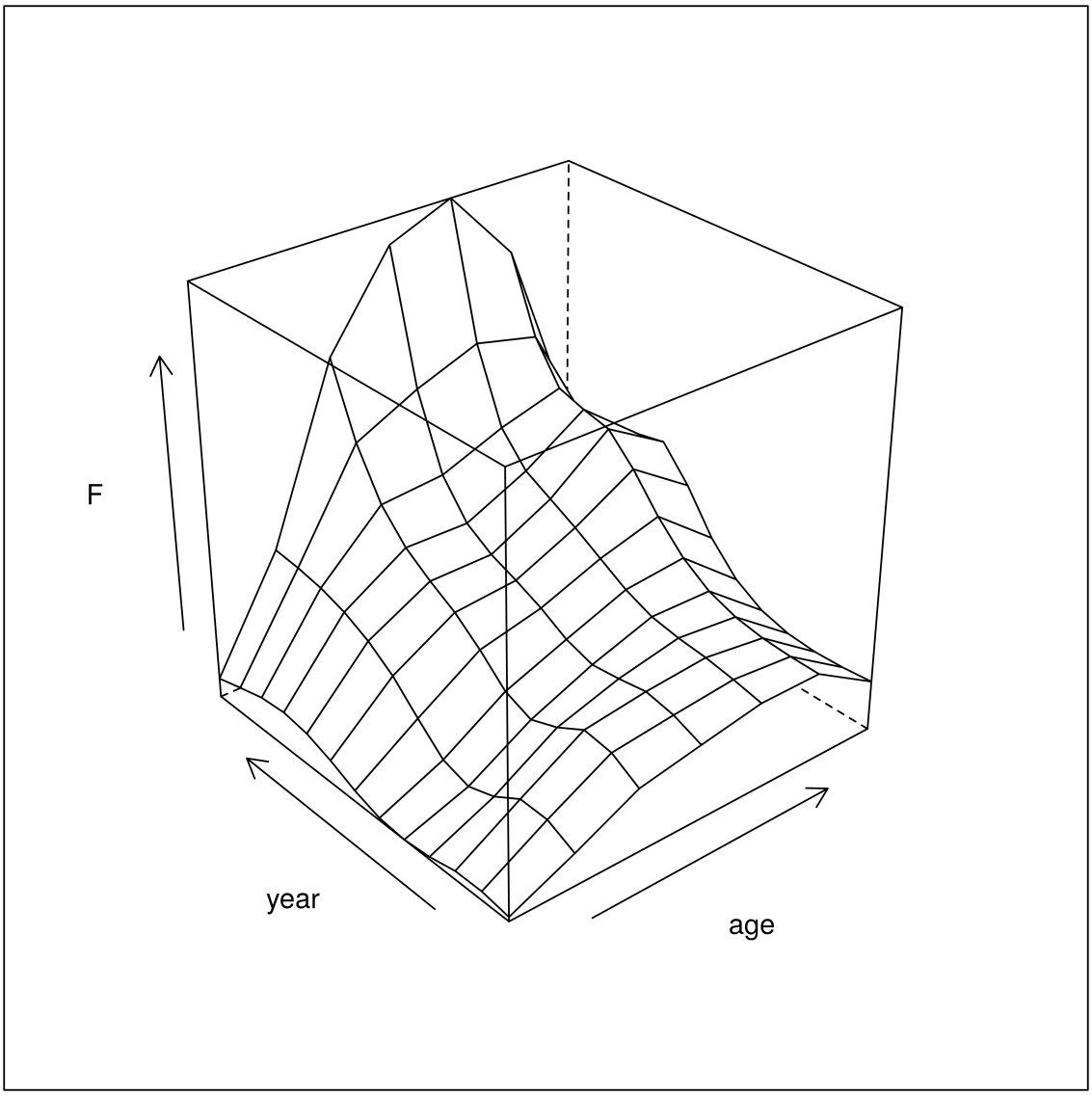

Figure 33: F-at-age estimate

```
plot(A.q4mc)
```

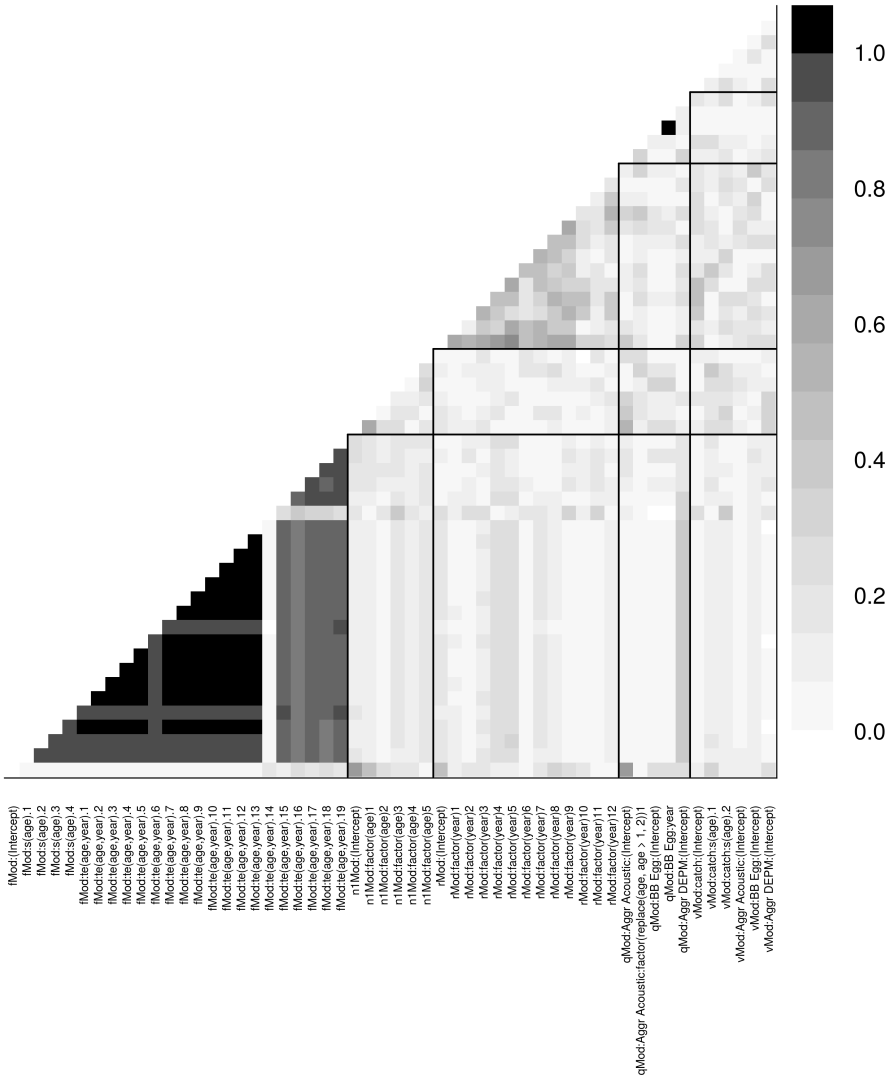

Figure 34: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(A.q4smc)
```

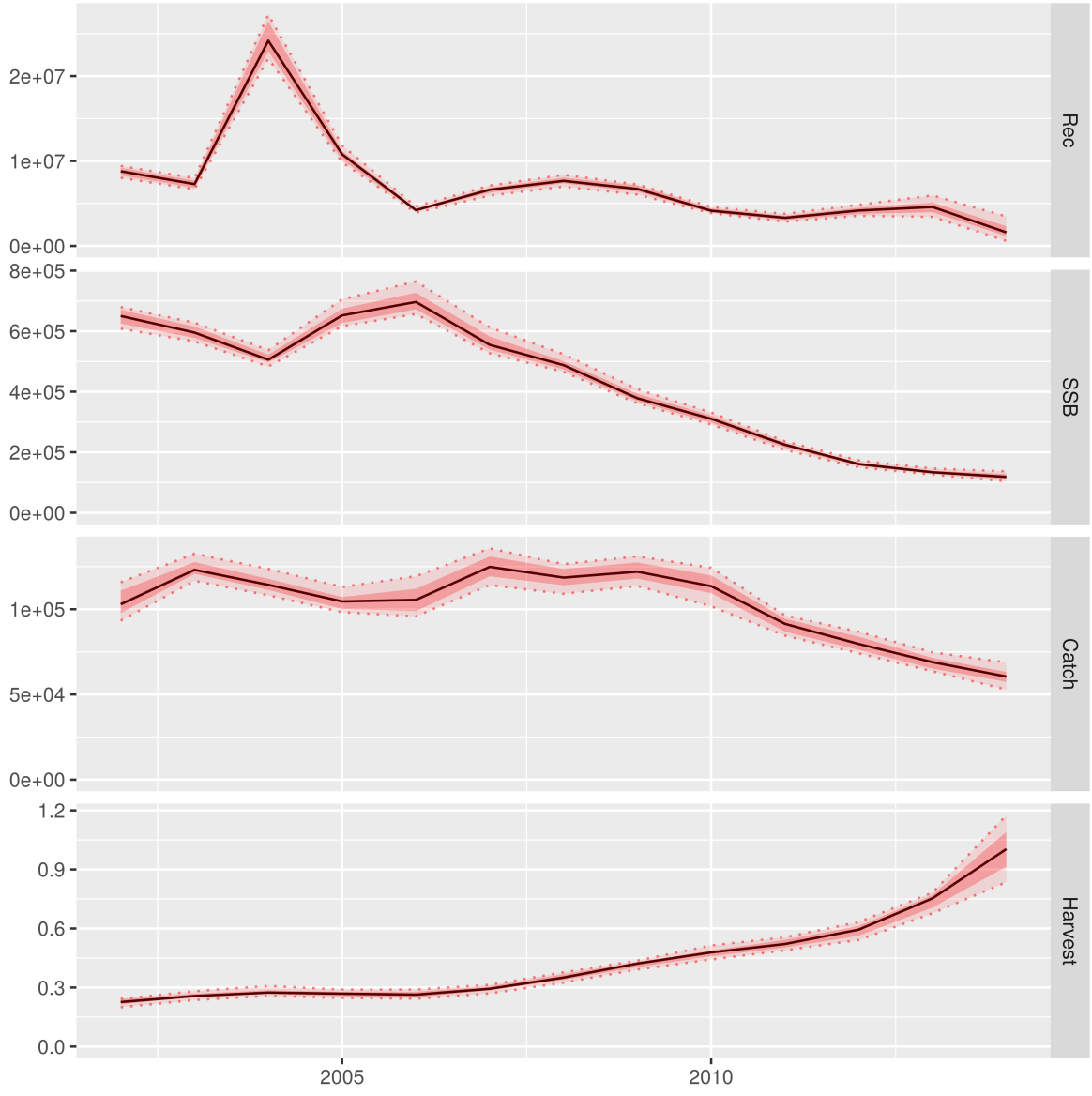

Figure 35: Summary plot

5.3.5 q option 5: constant, no overweighting of survey, no DEPM

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 7))
qmod <- list(~1)
A.q5f <- a4aSCA(A.stk, A.idx[1], fmodel = fmod, qmodel = qmod)
A.q5r <- residuals(A.q5f, A.stk, A.idx[1])
A.q5s <- A.stk + simulate(A.q5f, 500)
A.q5mc <- a4aSCA(A.stk, A.idx[1], fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
A.q5mcmc <- as.mcmc(A.q5mc)
A.q5smc <- A.stk + A.q5mc
```

```
plot(A.q5r)
```

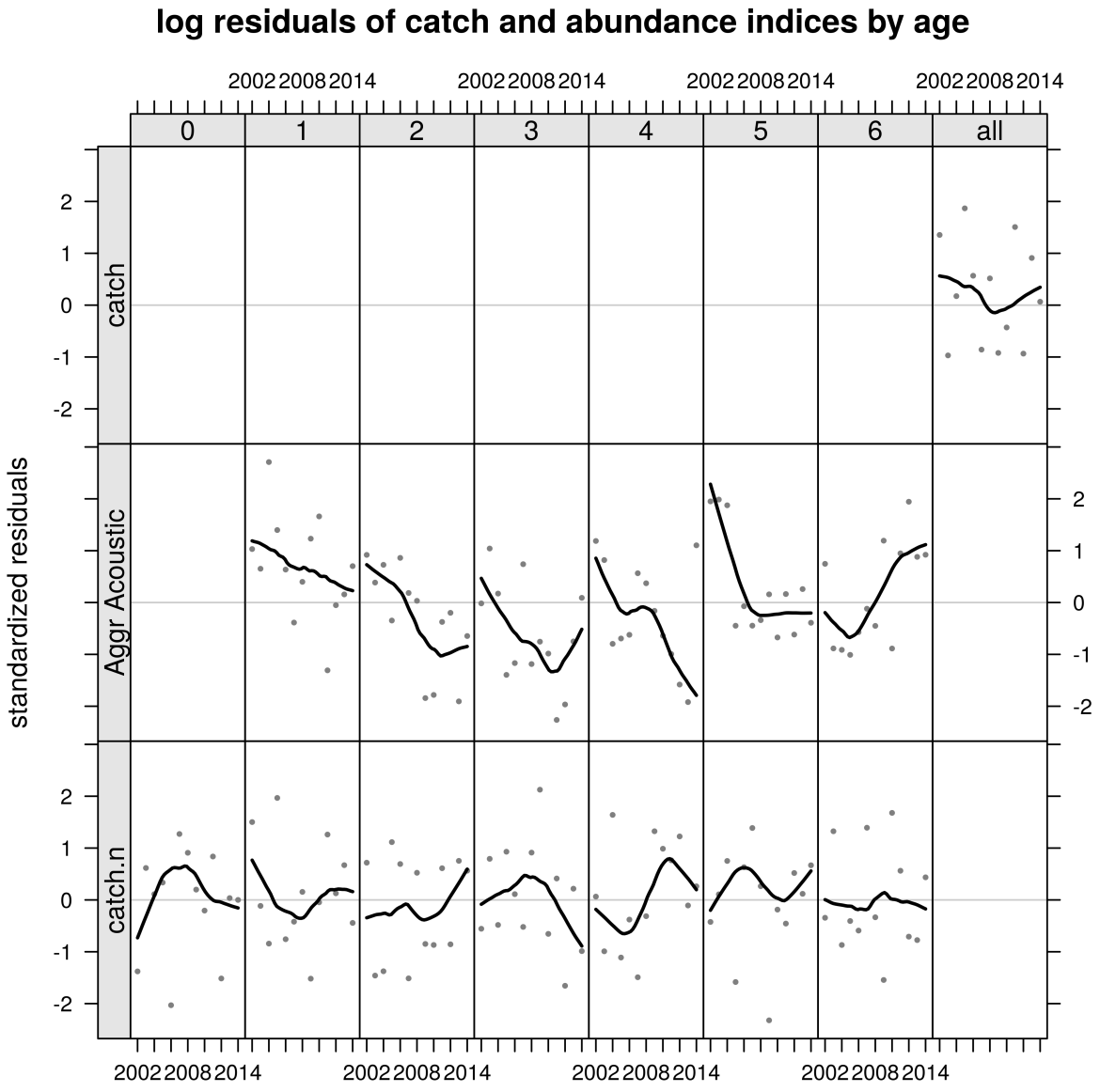

Figure 36: Residuals

```
plot(A.q5f, A.stk)
```

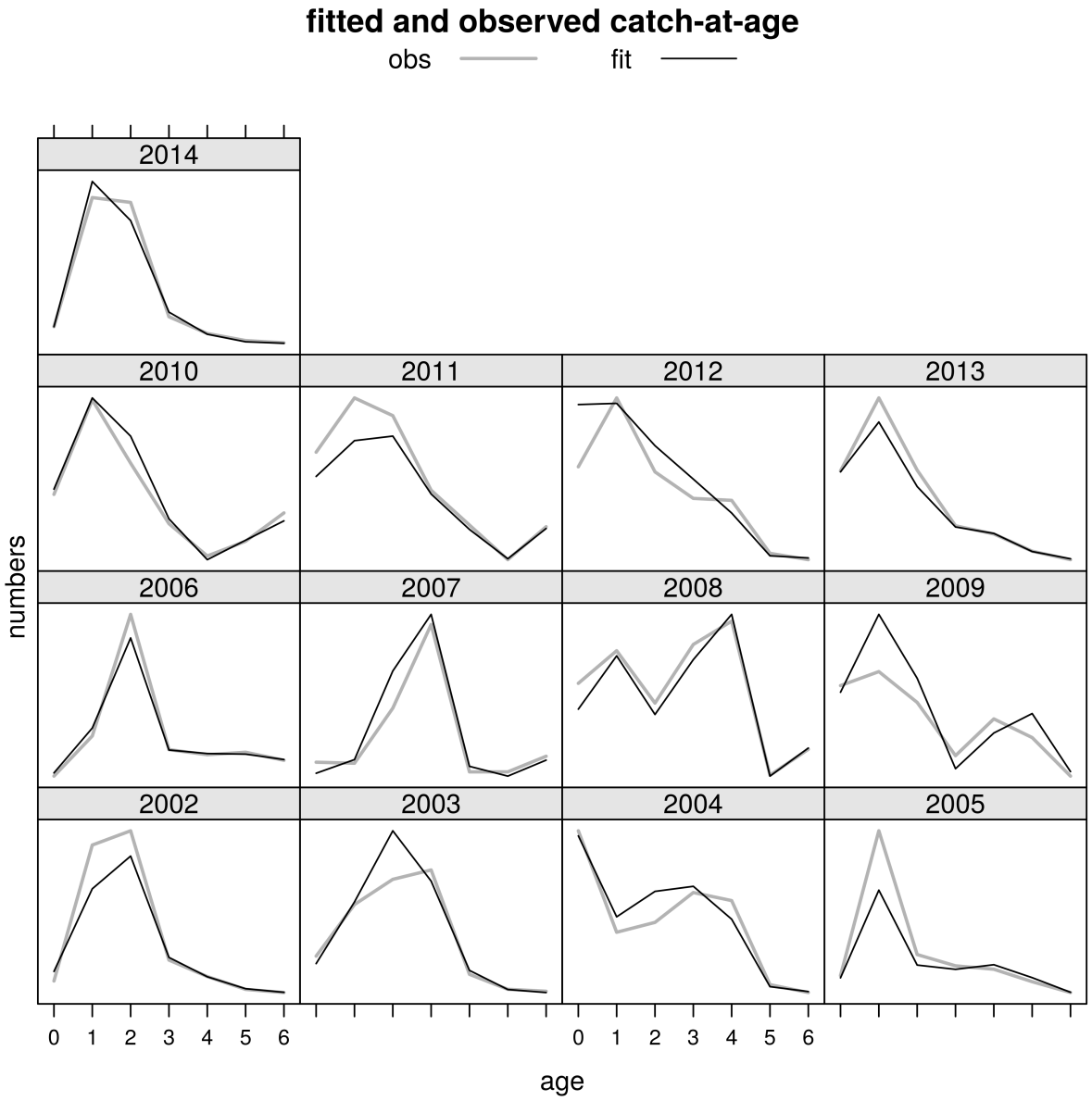

Figure 37: Catch-at-age predictions and observations

```
plot(A.q5f, A.idx[1])
```

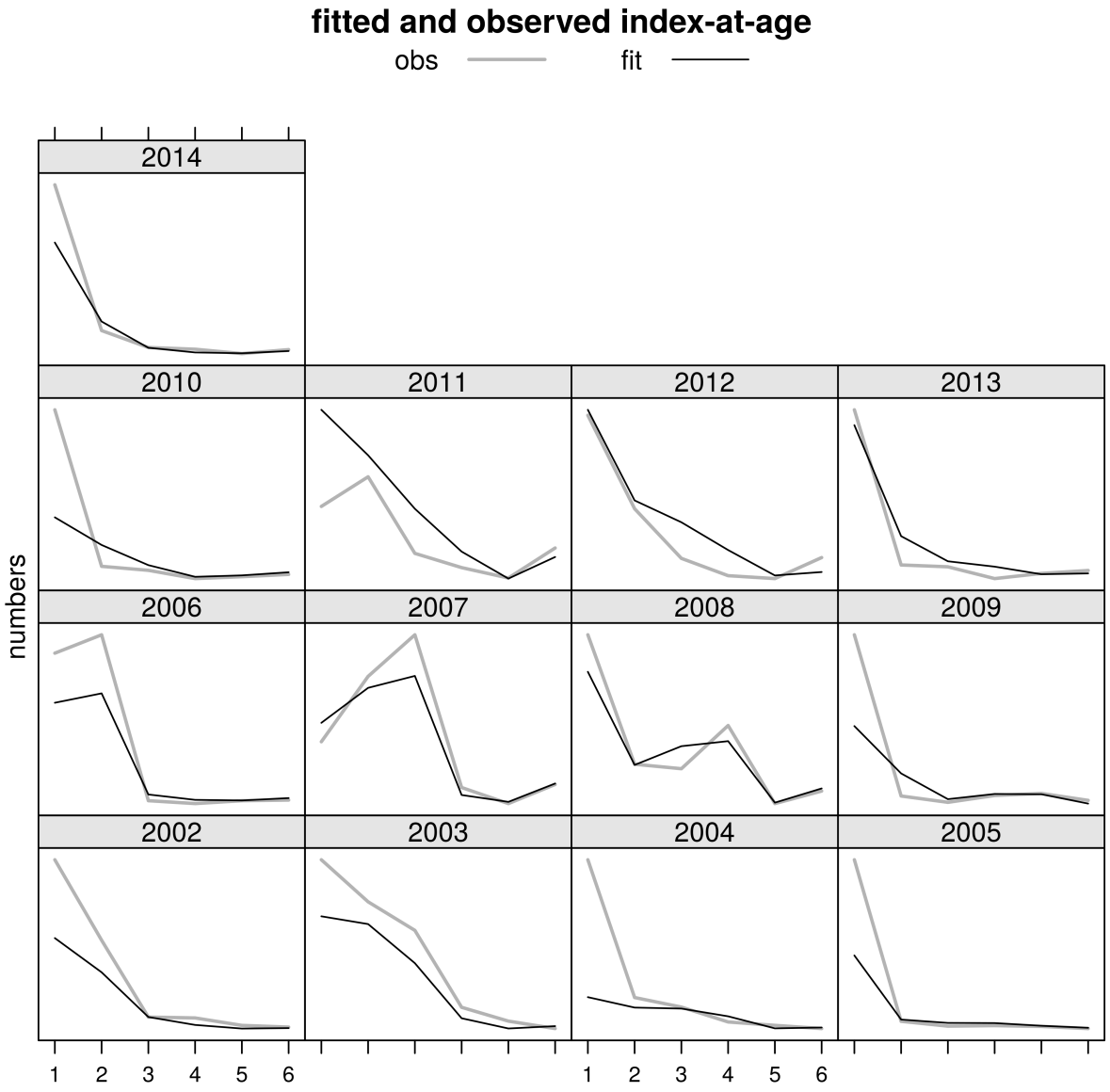

Figure 38: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(A.q5f))
```

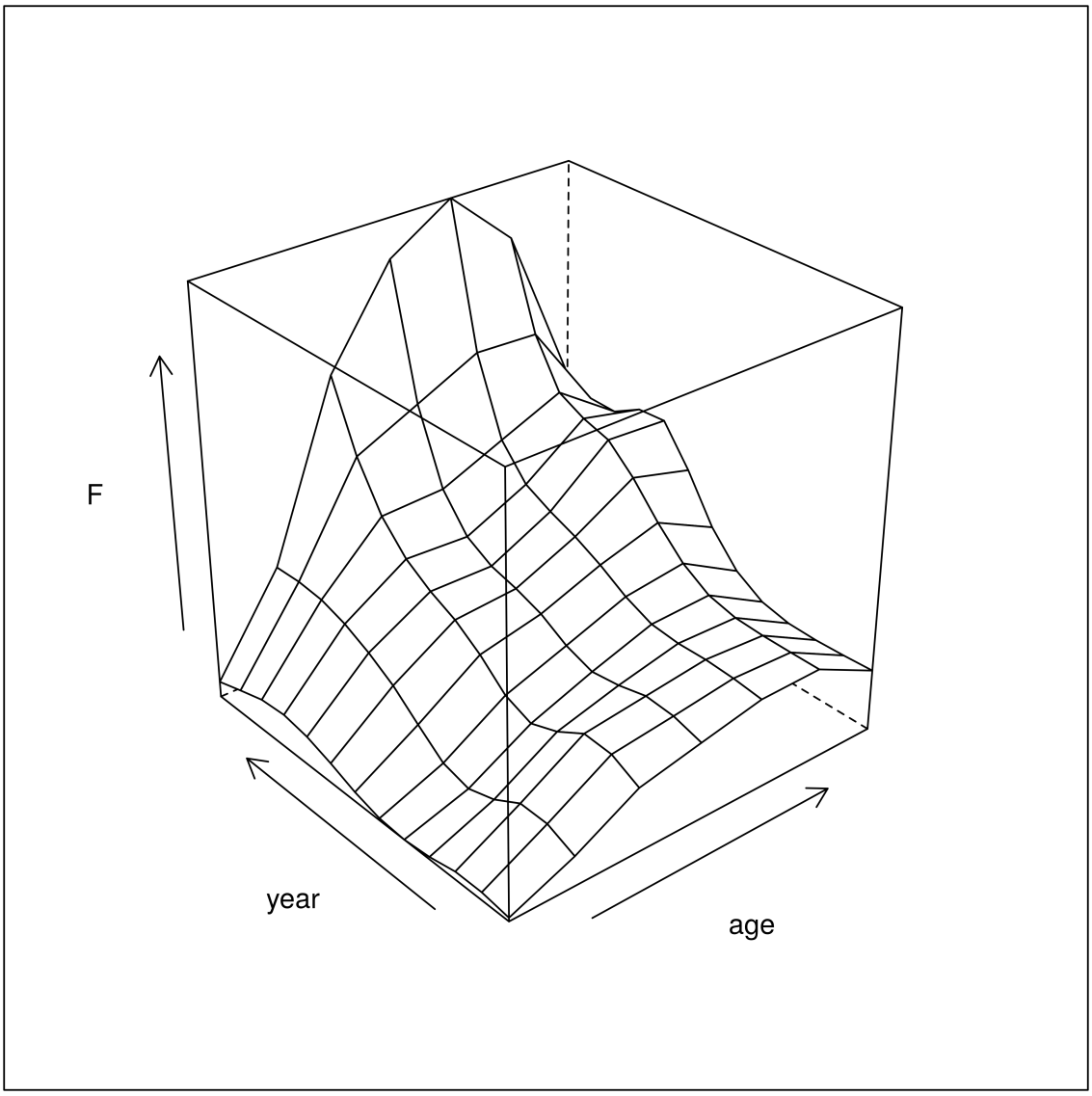

Figure 39: F-at-age estimate

```
plot(A.q5mc)
```

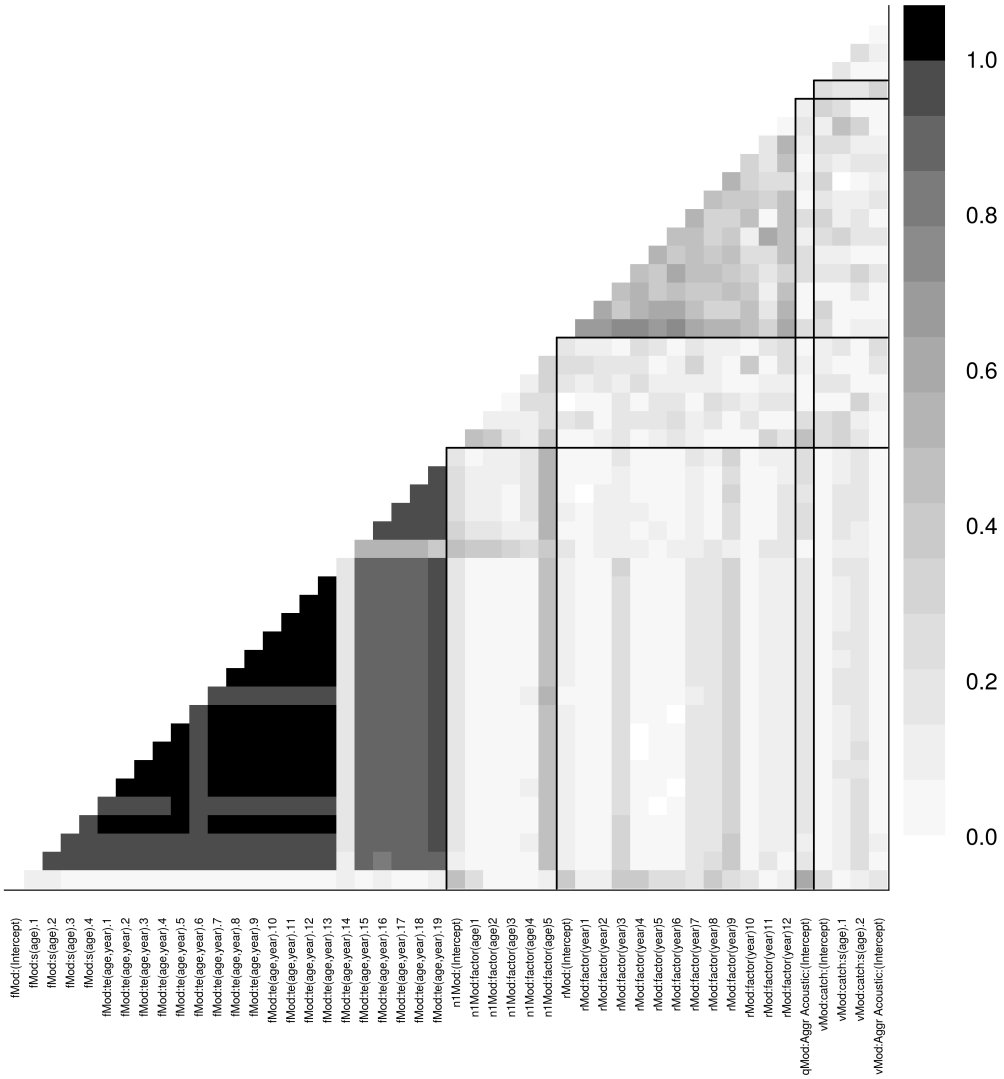

Figure 40: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(A.q5smc)
```

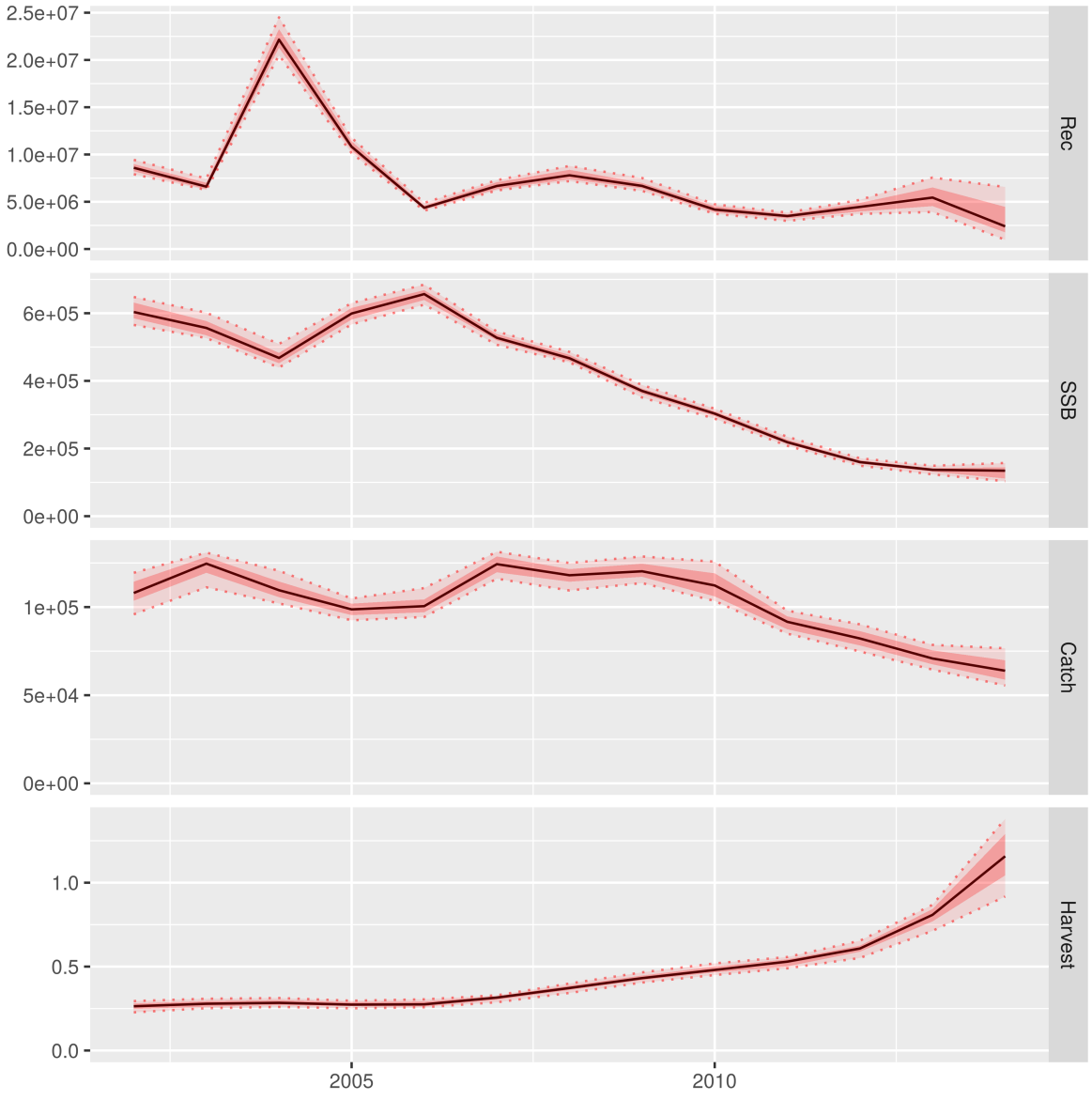

Figure 41: Summary plot

5.3.6 Comparison across assessments

```
plot(FLStocks(q1 = A.q1smc, q2 = A.q2smc, q3 = A.q3smc, q4 = A.q4smc,
    q5 = A.q5smc))
```

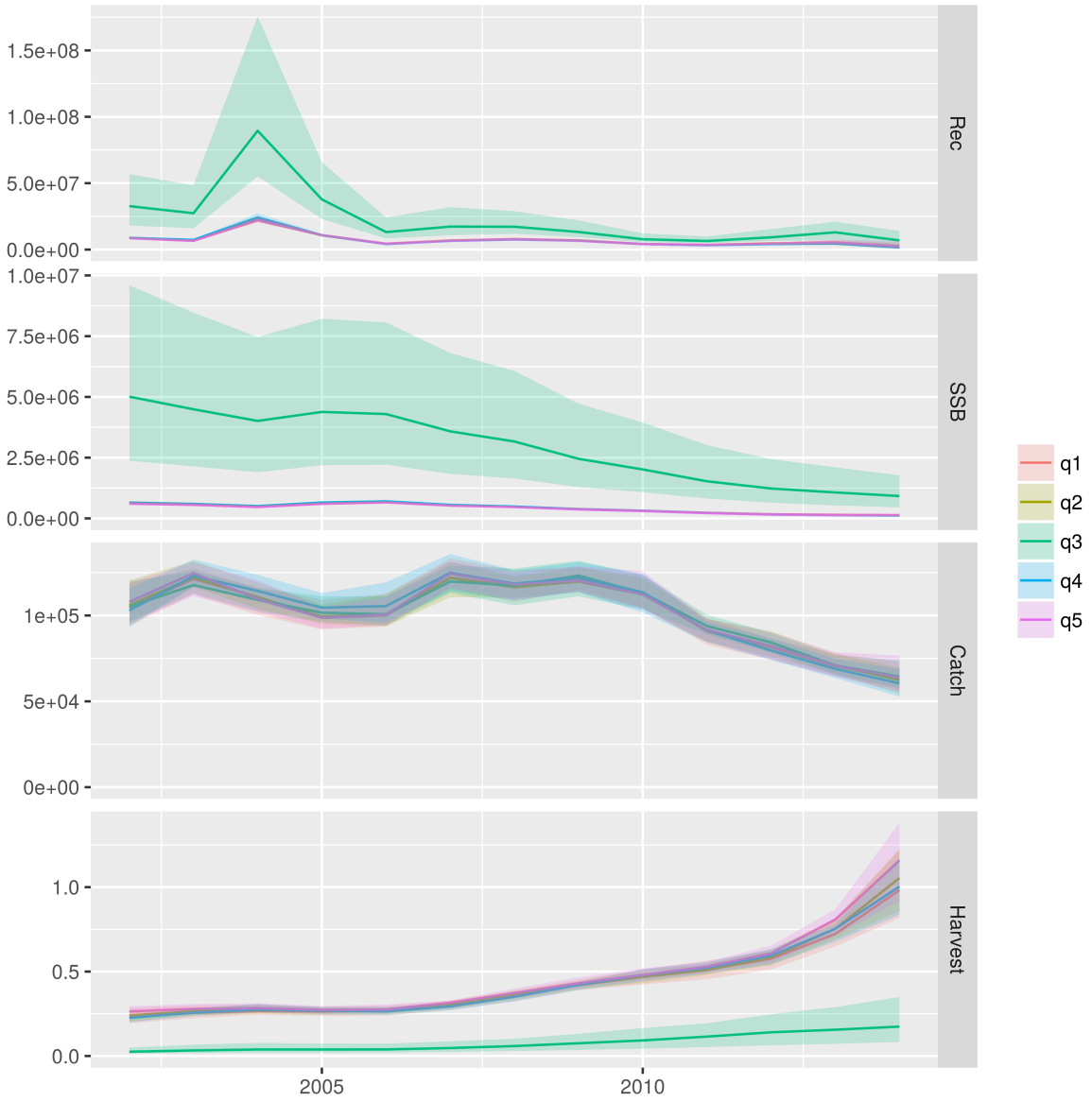

Figure 42: All assessments summary

5.3.7 Sensitivity to abundance indices

To test the sensitivity of the results to the abundance indices used a set of extra runs were performed with:

- q2extra - linear year effect on BB egg survey
- q2split - constant catchability accross all (disaggregated acoustic surveys and sum of DEPM)
- q2splity - linear year effect on BB and NW acoustic survey

```
A.idx2s <- FLIndices(BB1, NW1, S1, DP)
fmodel <- ~te(age, year, k = c(3, 7)) + s(age, k = 5)
q2extra <- list(~1, ~year, ~1)
q2split <- list(~1, ~1, ~1, ~1)
q2splity <- list(~year, ~year, ~1, ~1)
A.q2extramc <- a4aSCA(A.stk, A.idx, fmodel = fmodel, qmodel = q2extra,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.3))
A.q2splitmc <- a4aSCA(A.stk, A.idx2s, fmodel = fmodel, qmodel = q2split,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.3))
A.q2splitymc <- a4aSCA(A.stk, A.idx2s, fmodel = fmodel, qmodel = q2splity,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.3))
A.q2extrasmc <- A.stk + A.q2extramc
A.q2splitsmc <- A.stk + A.q2splitmc
A.q2splitysmc <- A.stk + A.q2splitymc
```

```
plot(FLStocks(q2 = A.q2smc, q2extra = A.q2extrasmc, q2split = A.q2splitsmc,
    q2splity = A.q2splitysmc))
```

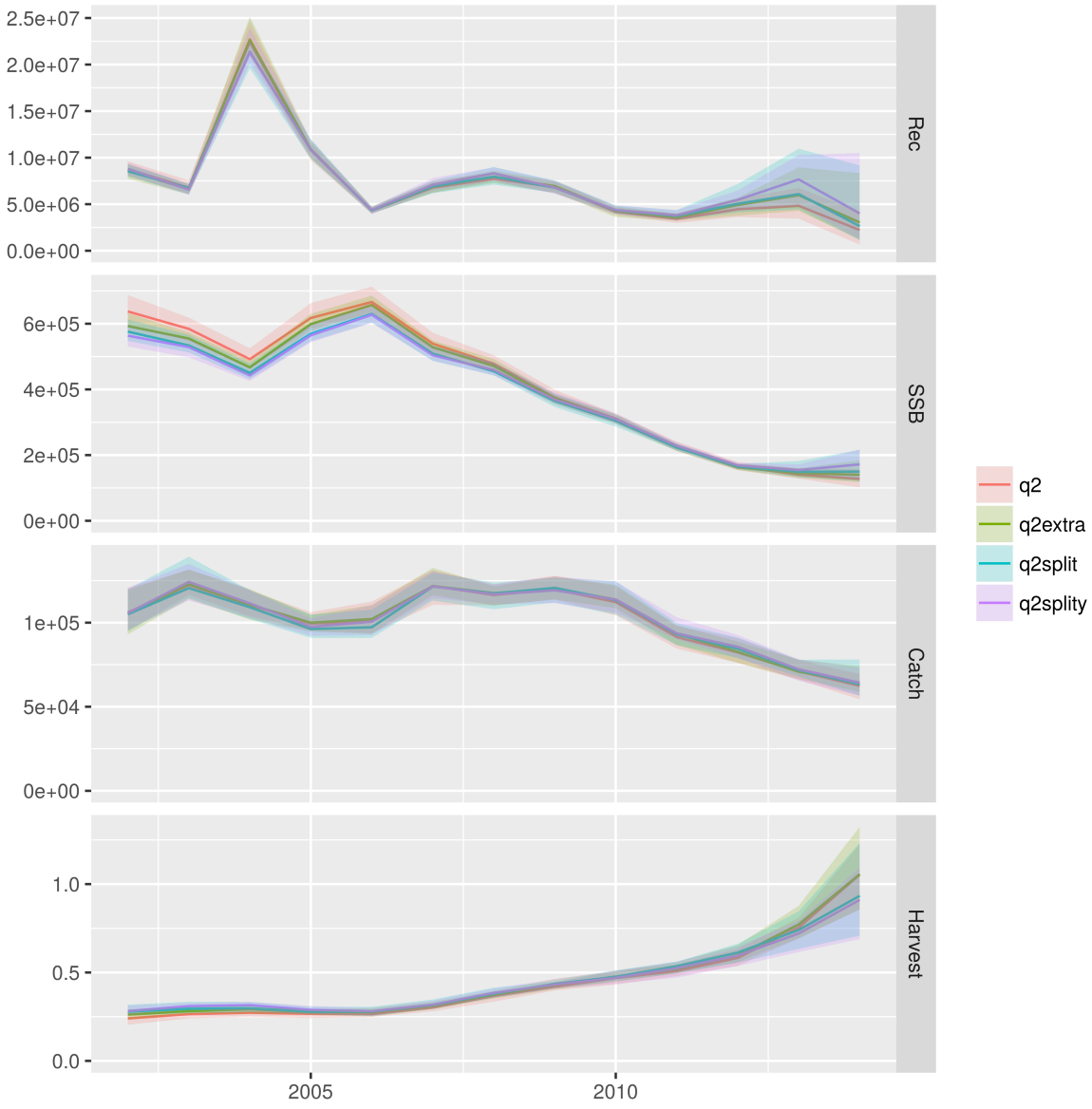

Figure 43: Summary of sensitivity analysis with catchability option 2

```
wireframe(data ~ year + age | qname, data = as.data.frame(FLQuants(q2 = harvest(A.q2smc),
    q2extra = harvest(A.q2extrasmc), q2split = harvest(A.q2splitsmc),
    q2splity = harvest(A.q2splitysmc))), as.table = T, zlim = c(0,
    1.3), zlab = "f")
```

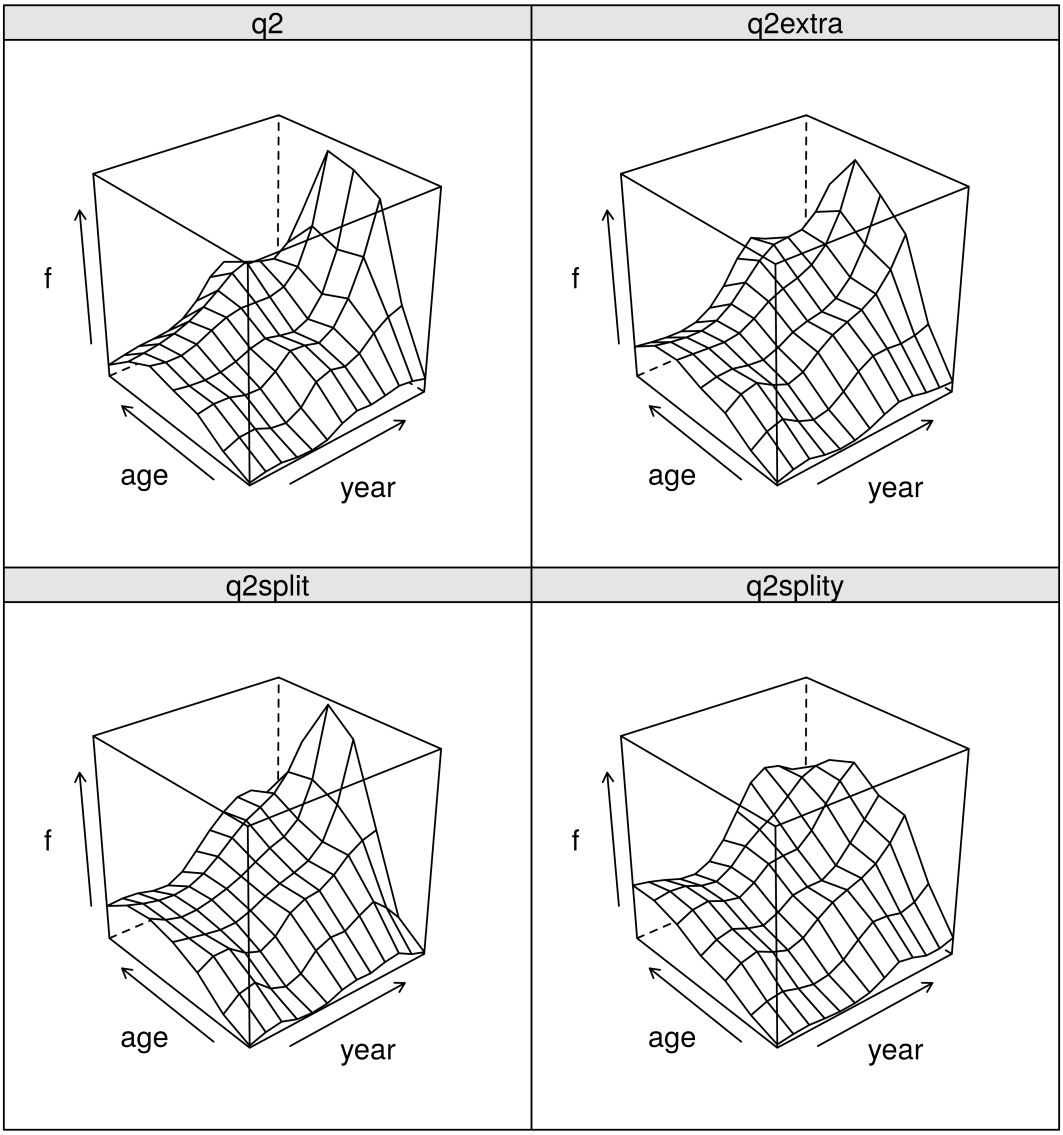

Figure 44: Fishing mortality surfaces sensitivity analysis with catchability option 2

5.4 The Bay of Biscay sub-unit

```
load("../analysis/BB/BBdata.RData")
BB.stk <- setPlusGroup(BB.stk, 6)
BB.idx[[1]] <- FLIndex(index = setPlusGroup(index(BB.idx[[1]]),
    6, by = "sum"))
range(BB.idx[[1]])[c("min", "max", "startf", "endf")] <- c(1,
    6, 4.8/12, 6/12)
range(BB.idx[[2]])[c("min", "max", "startf", "endf")] <- c(1,
    6, 5.1/12, 5.8/12)
mat(BB.stk)[2, ] <- 1
```

```
m.spwn(BB.stk) <- 0
harvest.spwn(BB.stk) <- 0
range(BB.stk)[c("minfbar", "maxfbar")] <- c(2, 5)
```

5.4.1 q option 1: smoother, no overweighting of survey

```
fmod <- ~te(age, year, k = c(6, 7))
qmod <- list(~s(age, k = 3), ~1)
BB.q1f <- a4aSCA(BB.stk, BB.idx, fmodel = fmod, qmodel = qmod)
BB.q1r <- residuals(BB.q1f, BB.stk, BB.idx)
BB.q1s <- BB.stk + simulate(BB.q1f, 500)
BB.q1mc <- a4aSCA(BB.stk, BB.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
BB.q1mcmc <- as.mcmc(BB.q1mc)
BB.q1smc <- BB.stk + BB.q1mc
```

```
plot(BB.q1r)
```

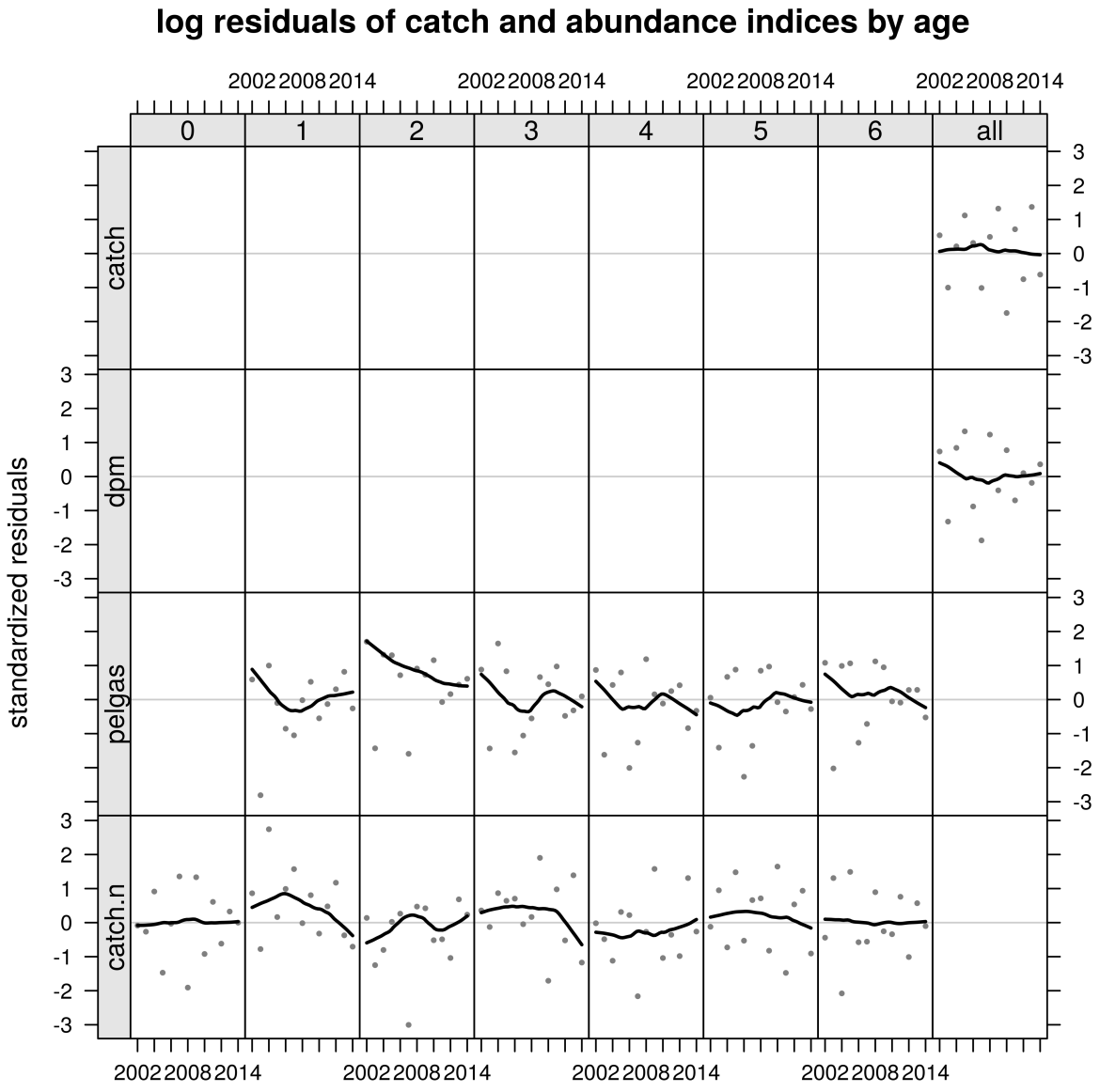

Figure 45: Residuals

```
plot(BB.q1f, BB.stk)
```

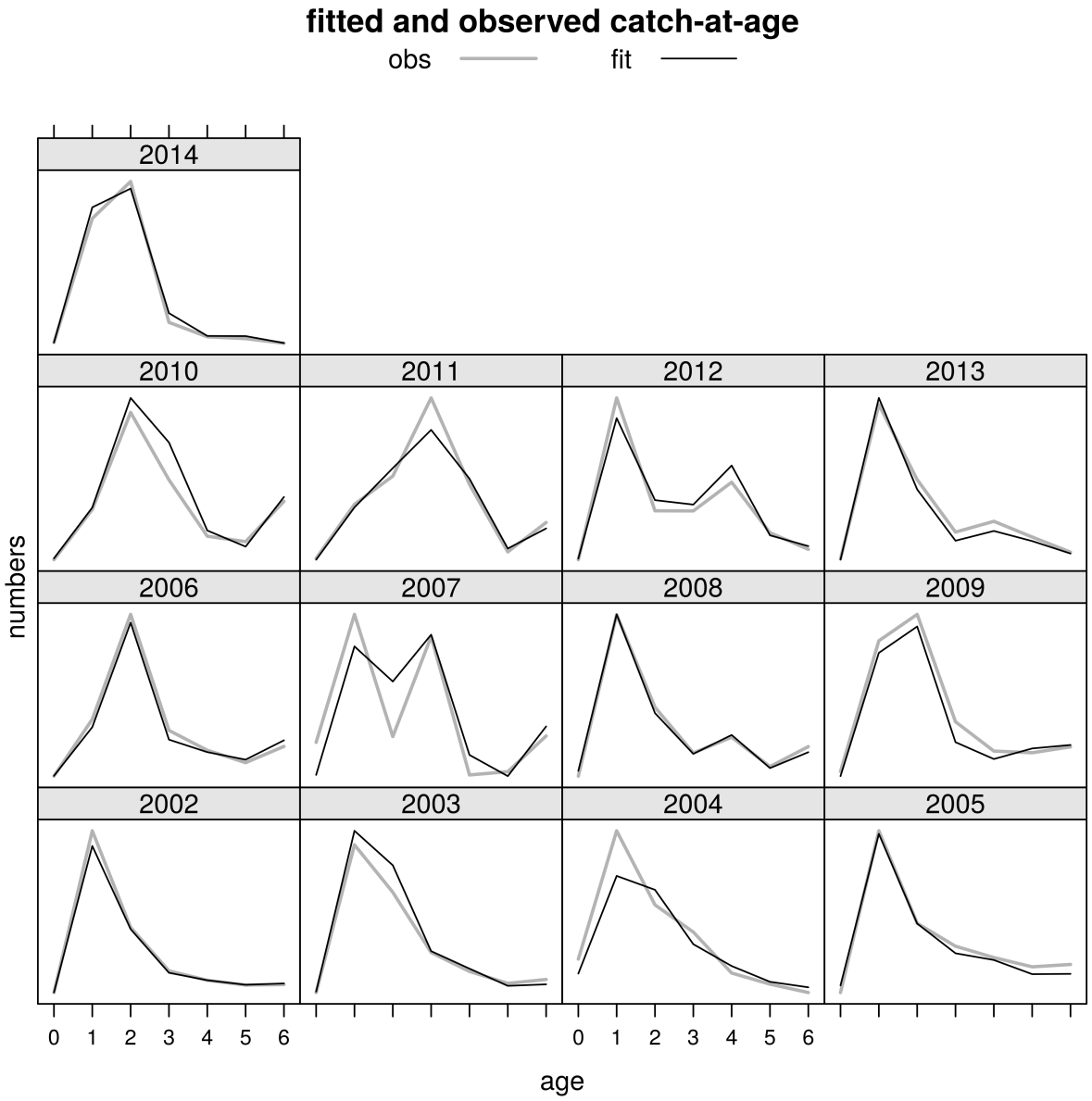

Figure 46: Catch-at-age predictions and observations

```
plot(BB.q1f, BB.idx[1])
```

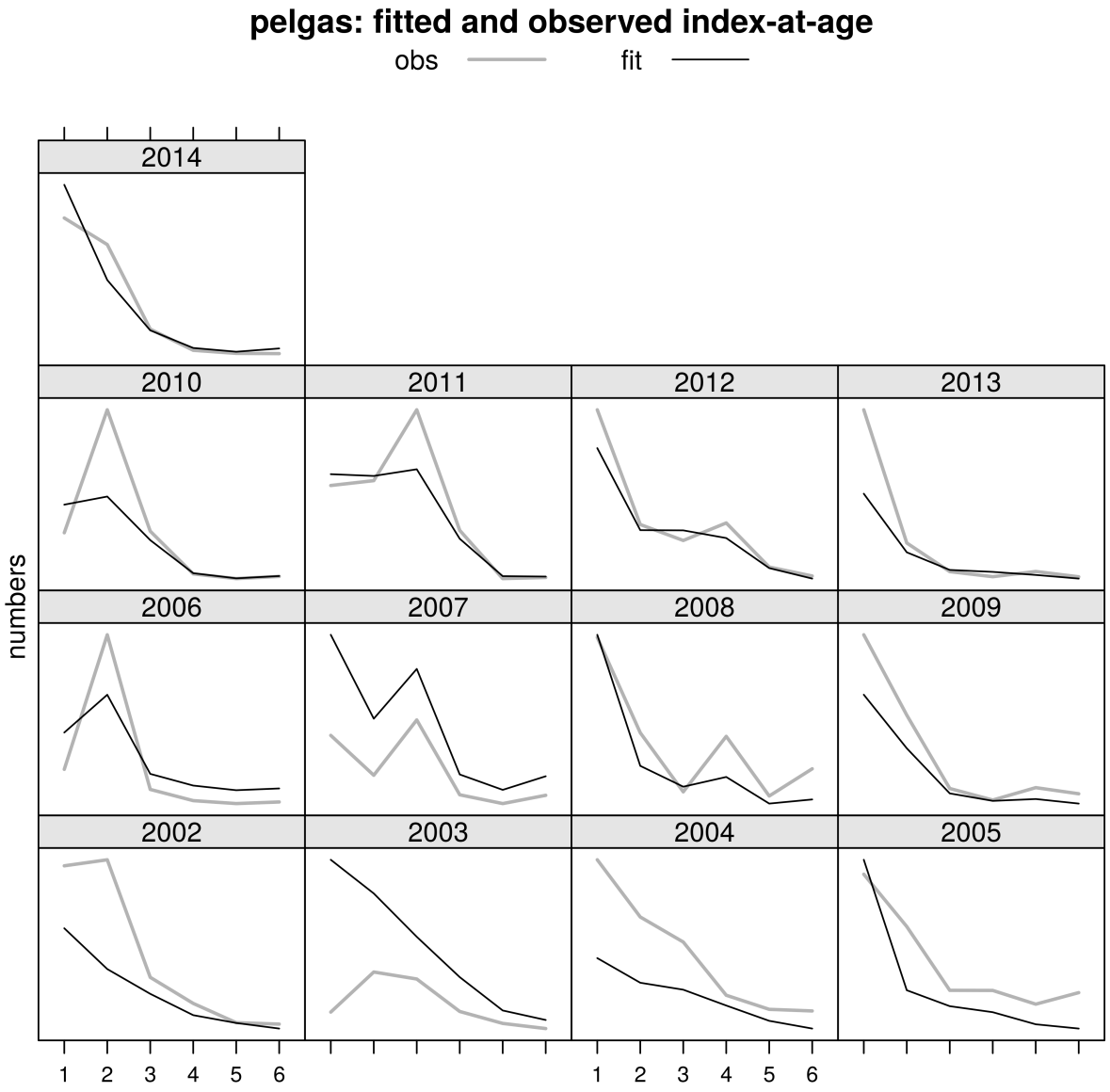

Figure 47: Index-at-age predictions and observations

```
wireframe(data ~ age + year, data = as.data.frame(harvest(BB.q1f)),
    drape = TRUE, main = "Fishing mortality")
```

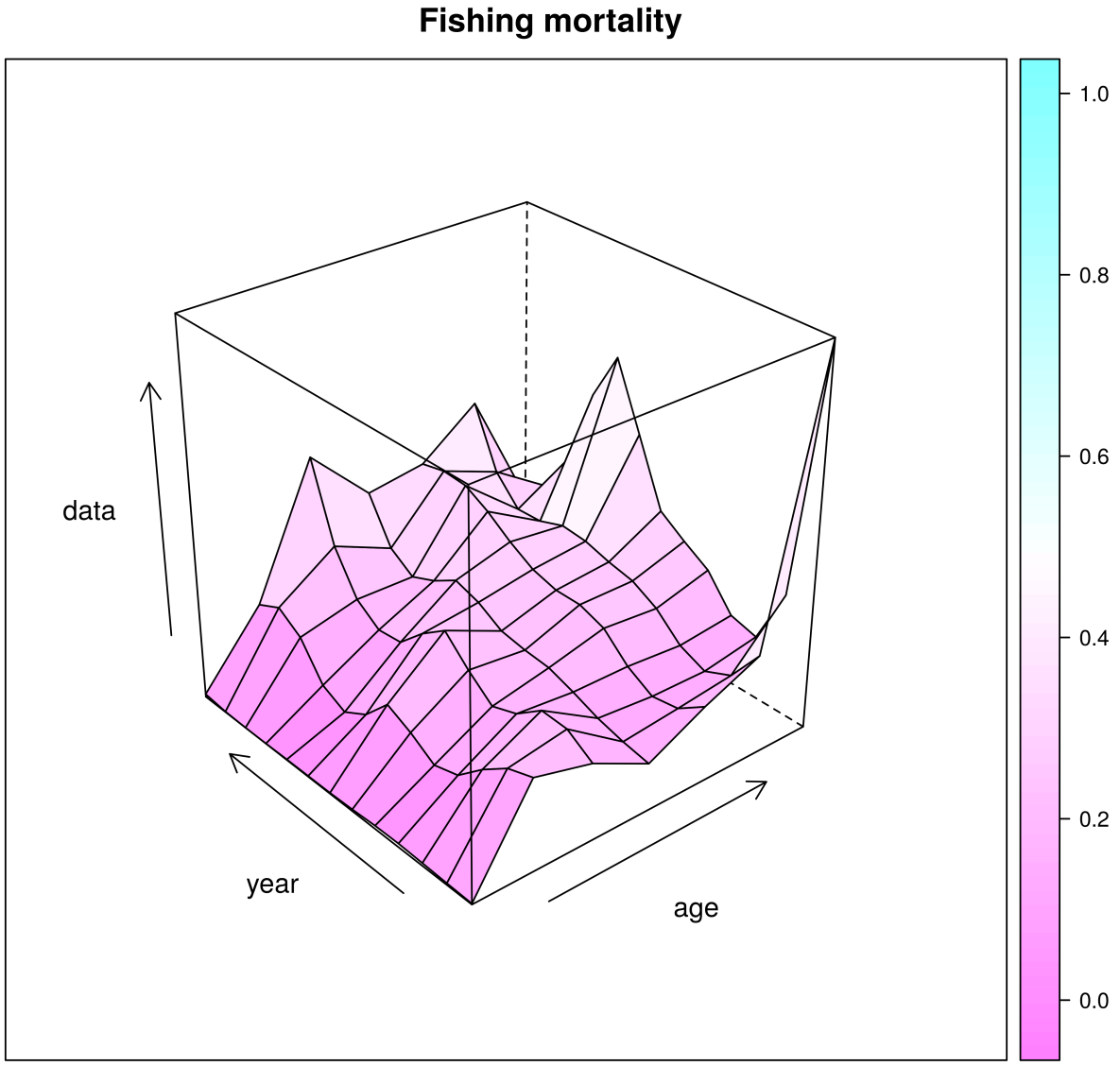

Figure 48: F-at-age estimates

```
wireframe(data ~ age + year, data = as.data.frame(predict(BB.q1f)$qmodel[[1]]),
    drape = TRUE, main = "q acoustic")
```

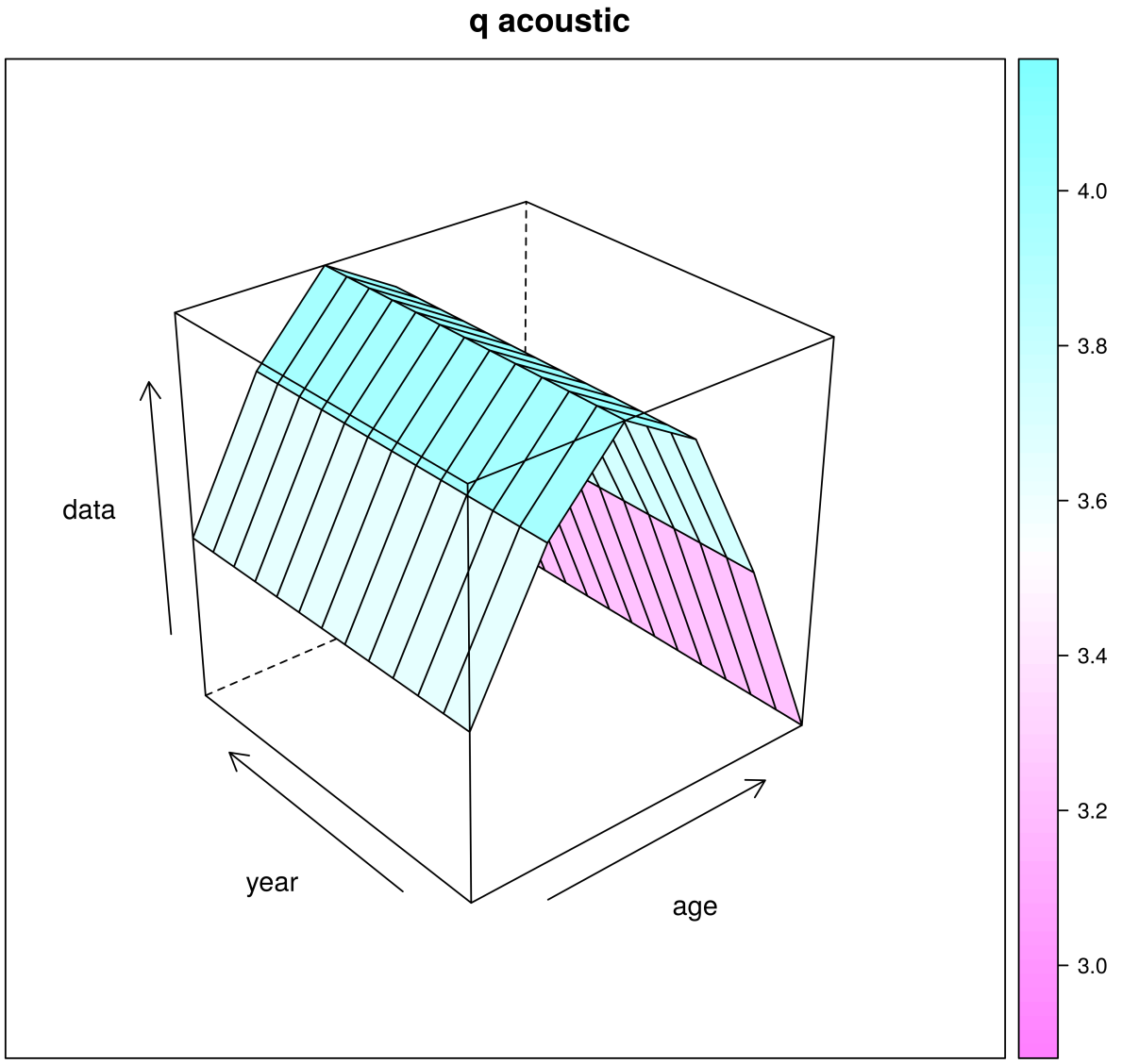

Figure 49: Catchability at age estimates

```
plot(BB.q1mc)
```

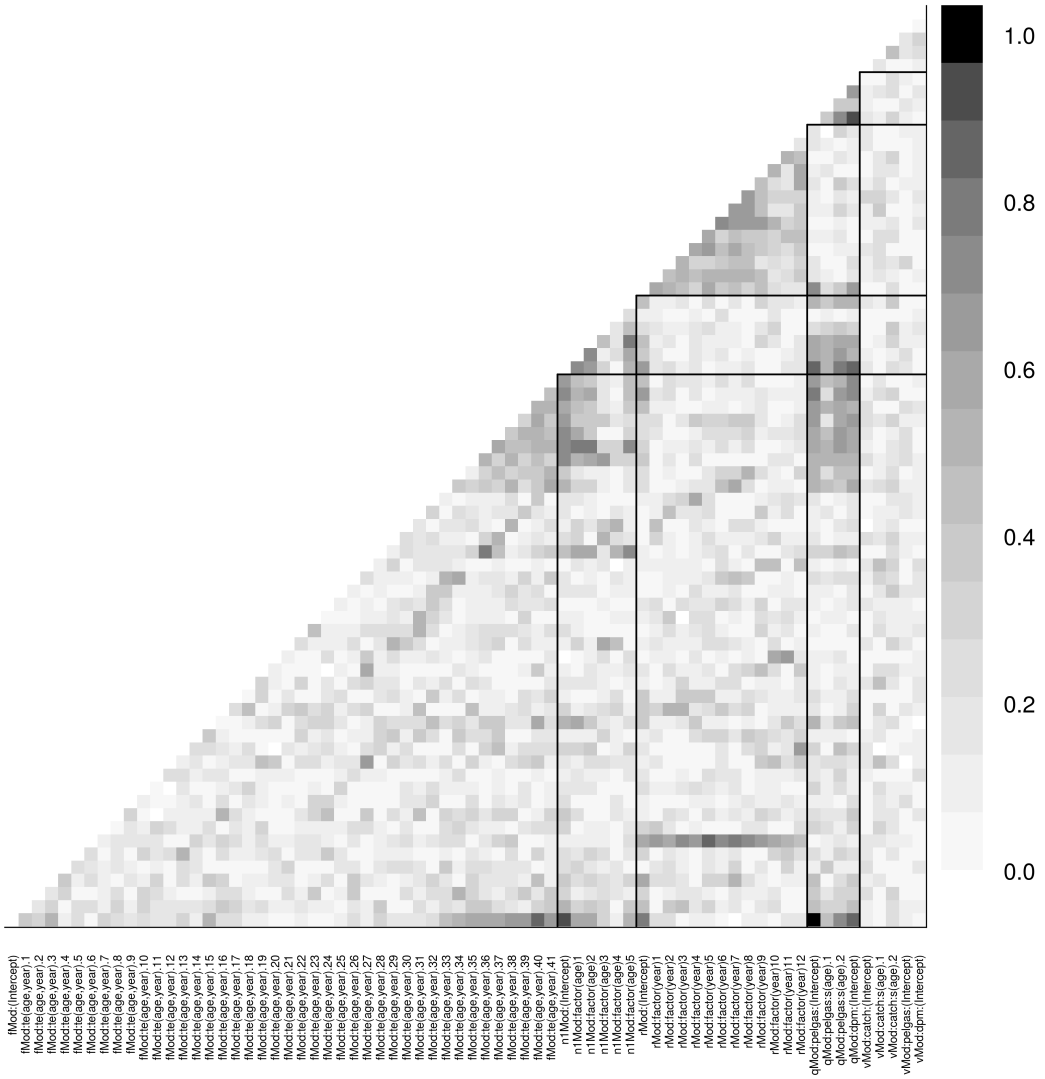

Figure 50: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(BB.q1smc)
```

Figure 51: Summary plot

5.4.2 q option 2: constant, no overweighting of survey

```
fmod <- ~te(age, year, k = c(6, 7))
qmod <- list(~1, ~1)
BB.q2f <- a4aSCA(BB.stk, BB.idx, fmodel = fmod, qmodel = qmod)
BB.q2r <- residuals(BB.q2f, BB.stk, BB.idx)
BB.q2s <- BB.stk + simulate(BB.q2f, 500)
BB.q2mc <- a4aSCA(BB.stk, BB.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
BB.q2mcmc <- as.mcmc(BB.q2mc)
BB.q2smc <- BB.stk + BB.q2mc
```

```
plot(BB.q2r)
```

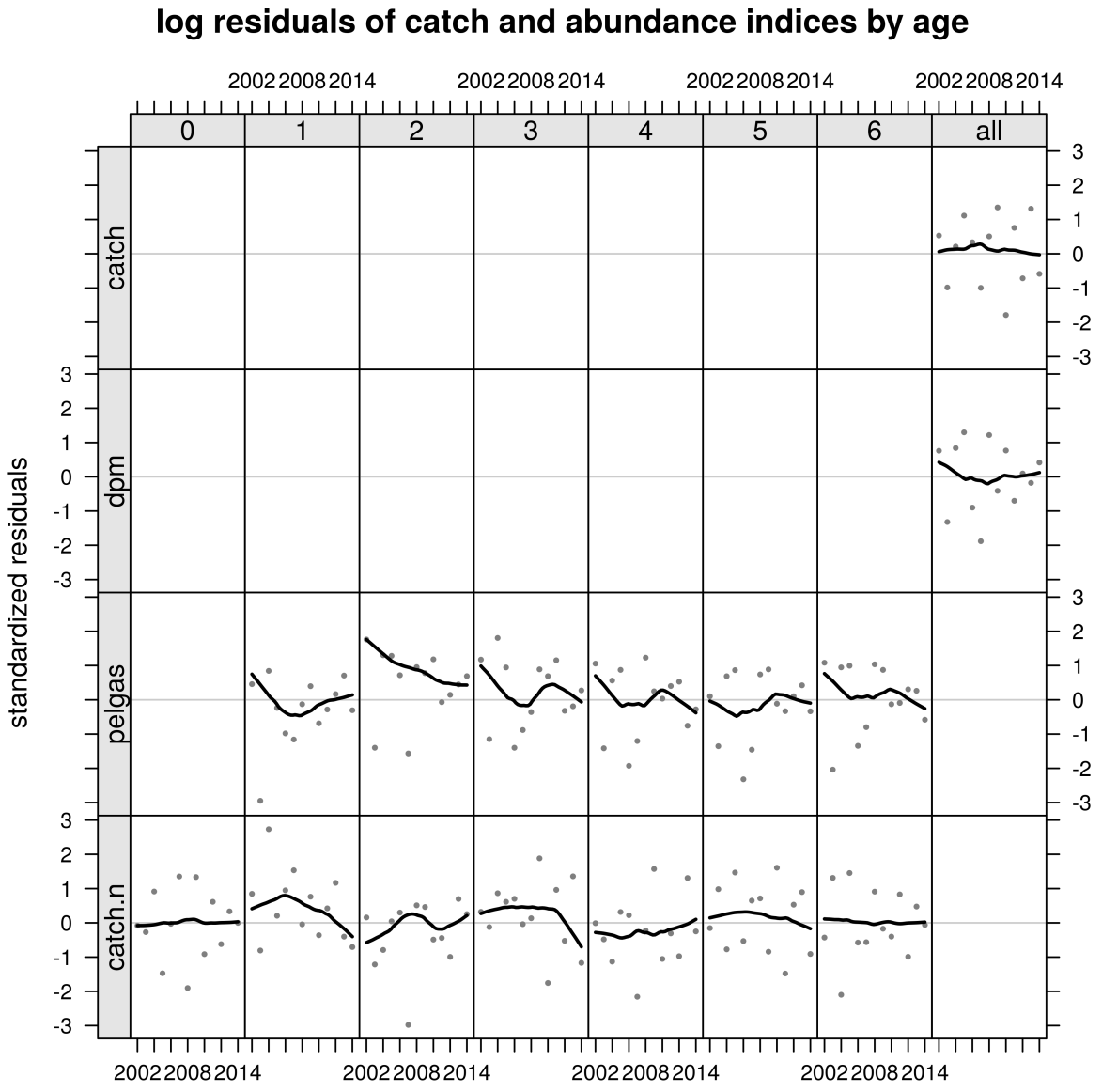

Figure 52: Residuals

```
plot(BB.q2f, BB.stk)
```

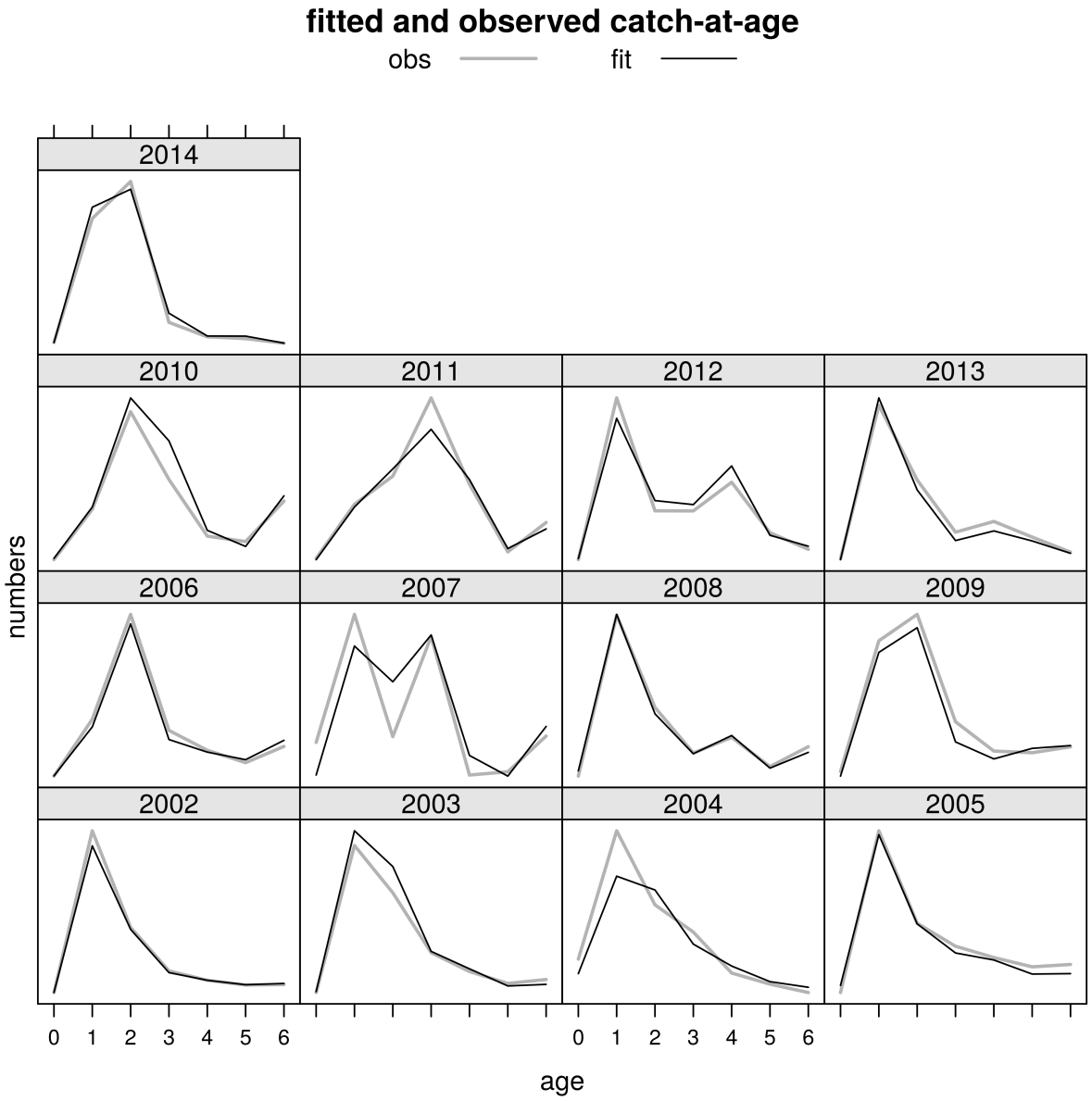

Figure 53: Catch-at-age predictions and observations

```
plot(BB.q2f, BB.idx[1])
```

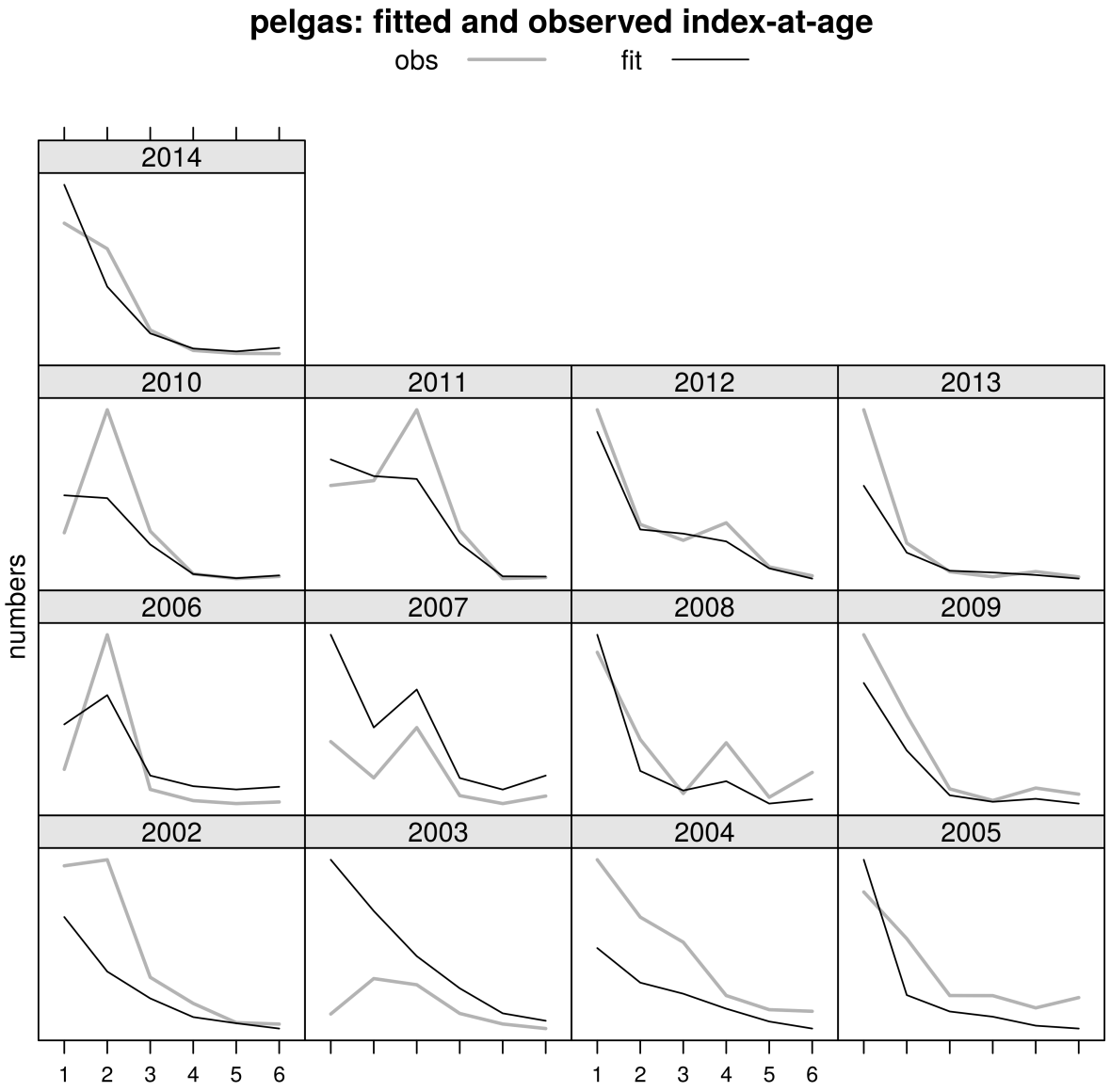

Figure 54: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(BB.q2f))
```

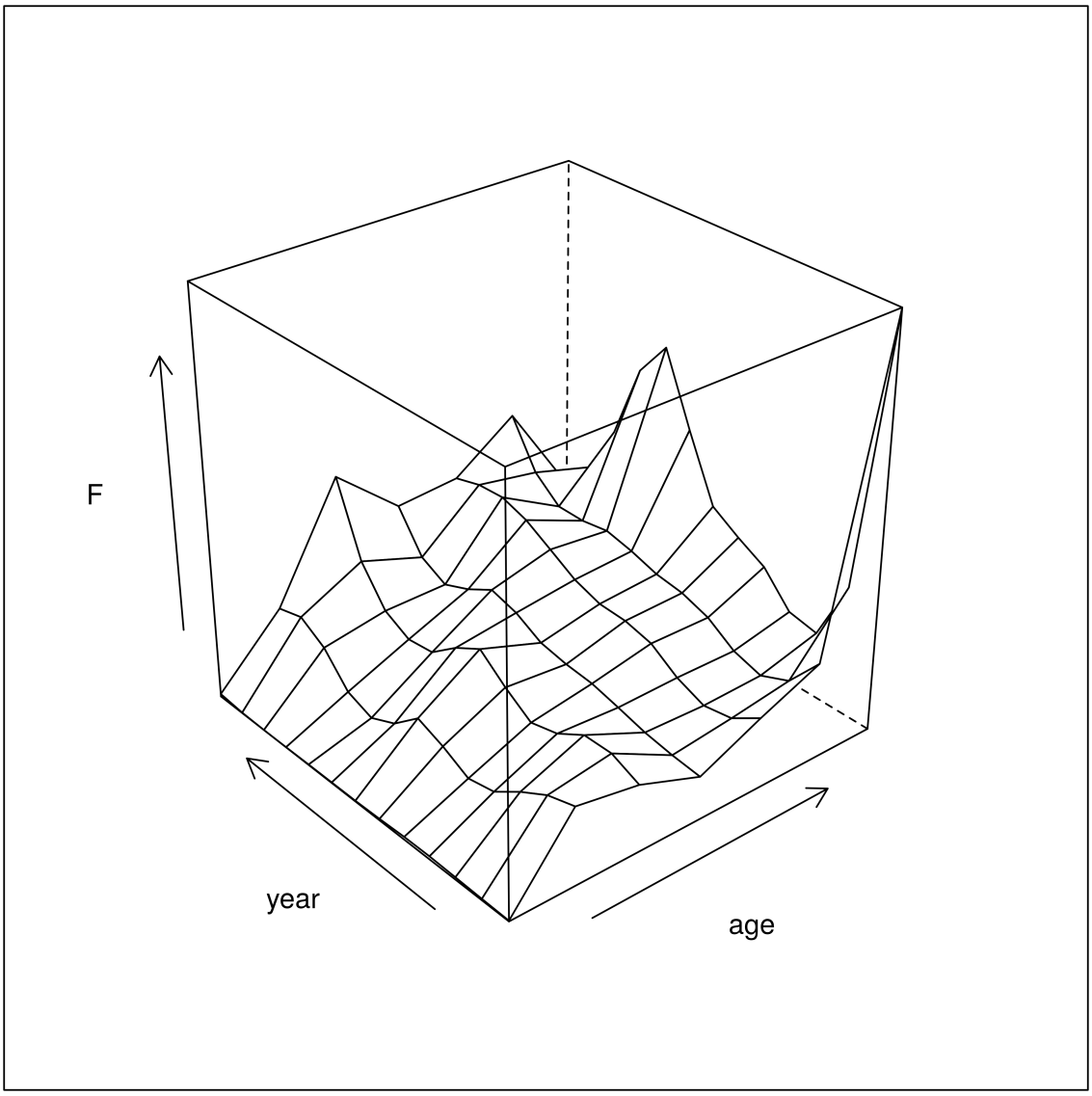

Figure 55: F-at-age estimate

```
plot(BB.q2mc)
```

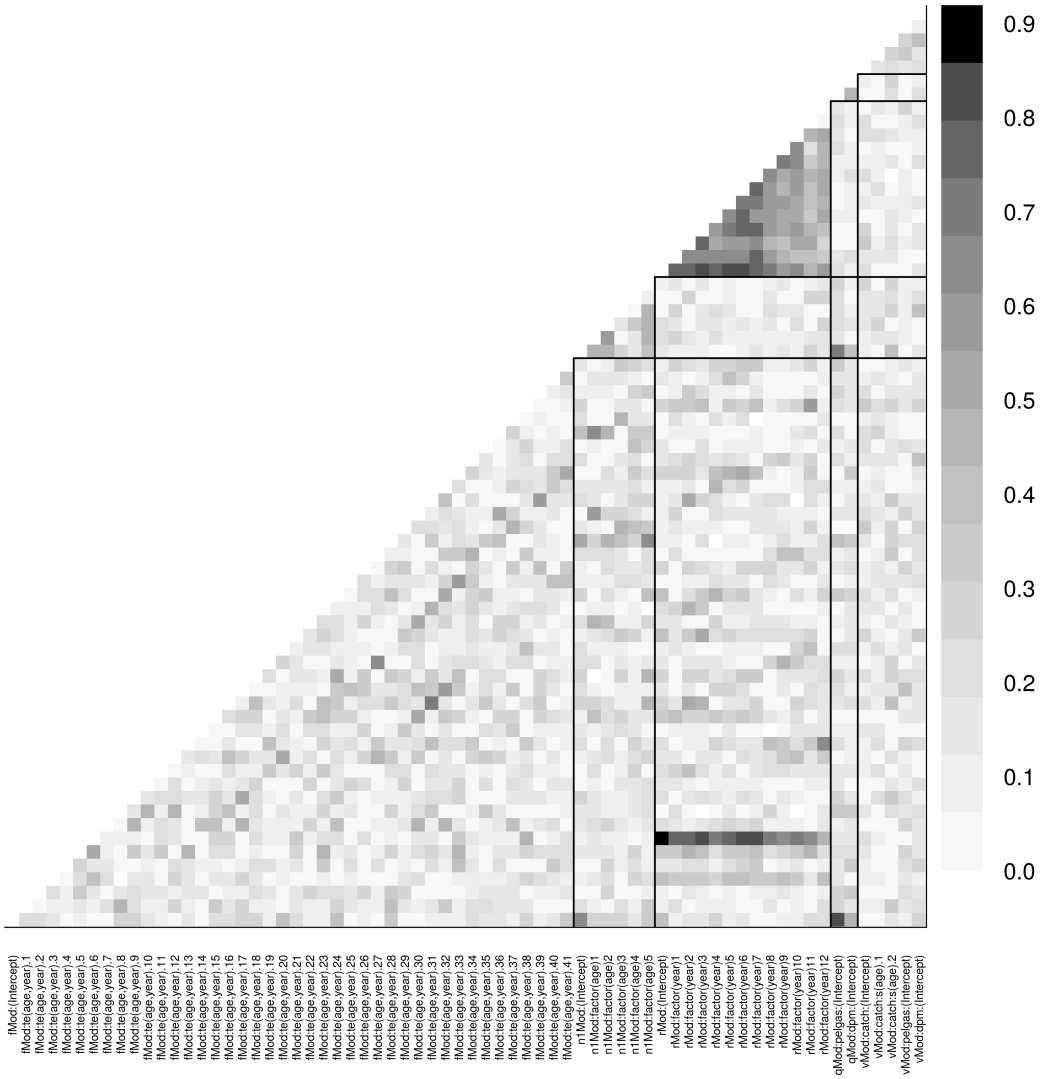

Figure 56: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(BB.q2smc)
```

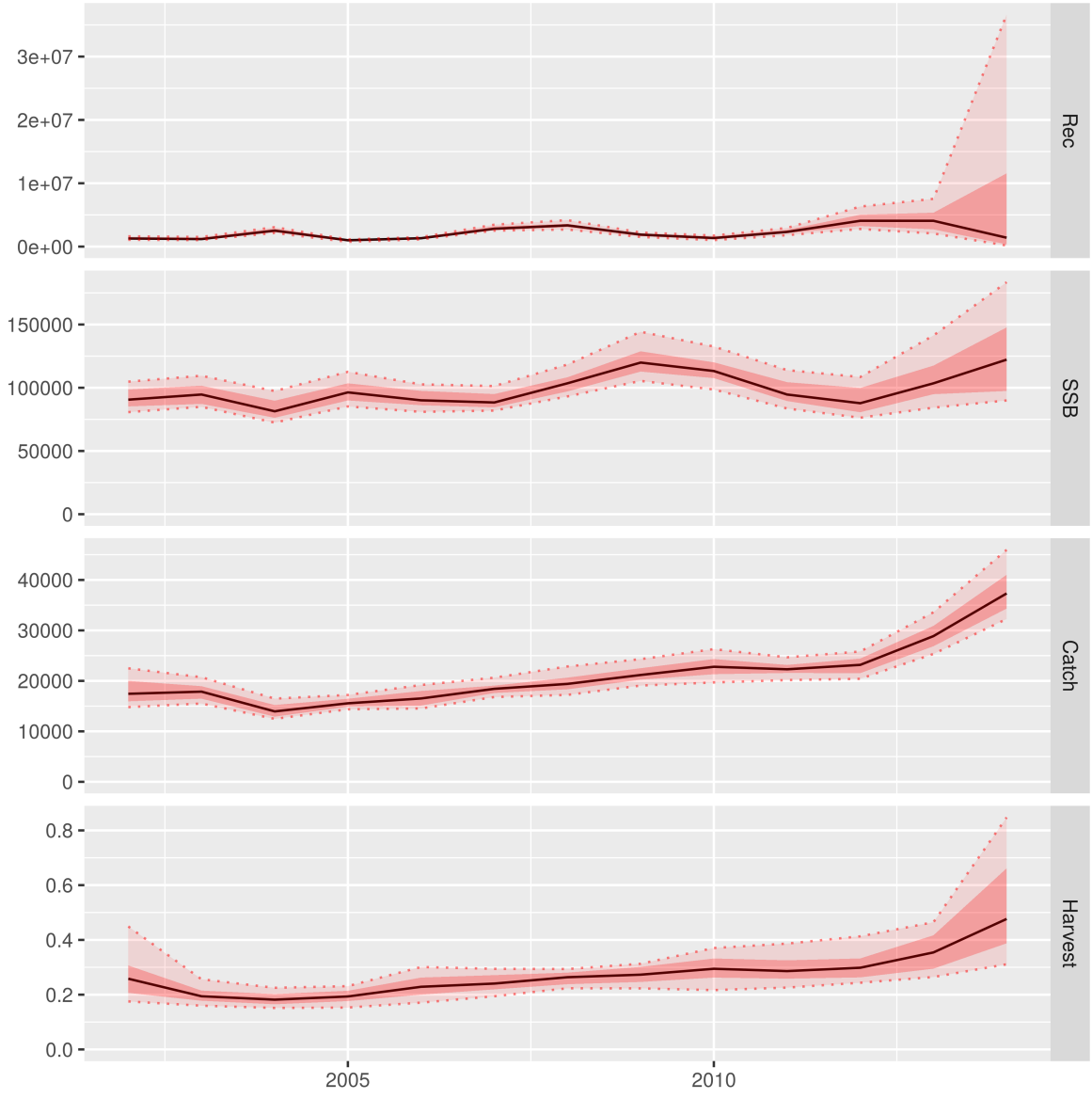

Figure 57: Summary plot

5.4.3 q option 3: smoother, survey overweighting

```
fmod <- ~te(age, year, k = c(6, 7))
qmod <- list(~s(age, k = 3), ~1)
BB.idx2 <- BB.idx
index.var(BB.idx2[[1]]) <- 0.5
BB.q3f <- a4aSCA(BB.stk, BB.idx2, fmodel = fmod, qmodel = qmod)
BB.q3r <- residuals(BB.q3f, BB.stk, BB.idx2)
BB.q3s <- BB.stk + simulate(BB.q3f, 500)
BB.q3mc <- a4aSCA(BB.stk, BB.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
BB.q3mcmc <- as.mcmc(BB.q3mc)
BB.q3smc <- BB.stk + BB.q3mc
```

```
plot(BB.q3r)
```

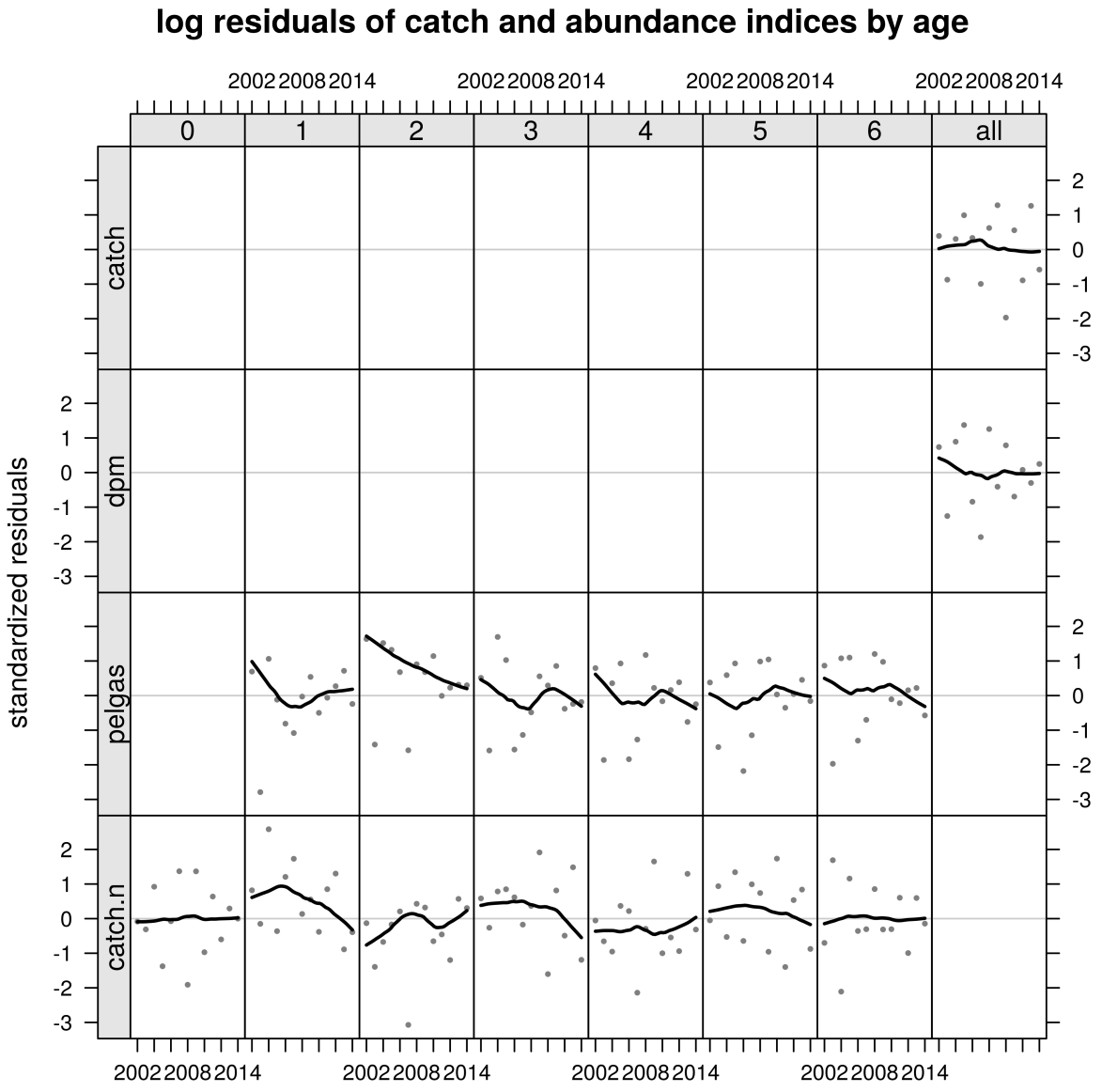

Figure 58: Residuals

```
plot(BB.q3f, BB.stk)
```

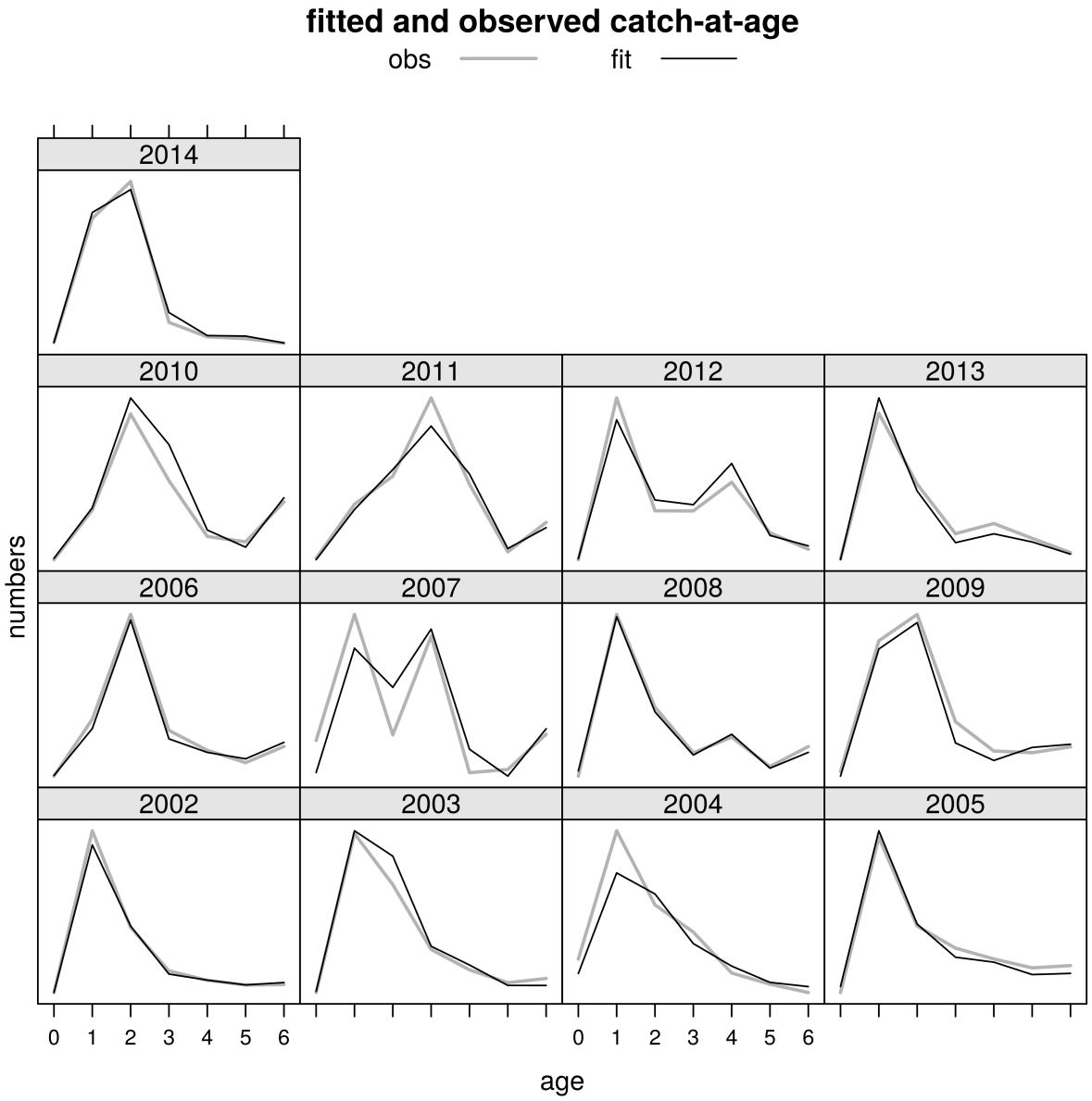

Figure 59: Catch-at-age predictions and observations

```
plot(BB.q3f, BB.idx2[1])
```

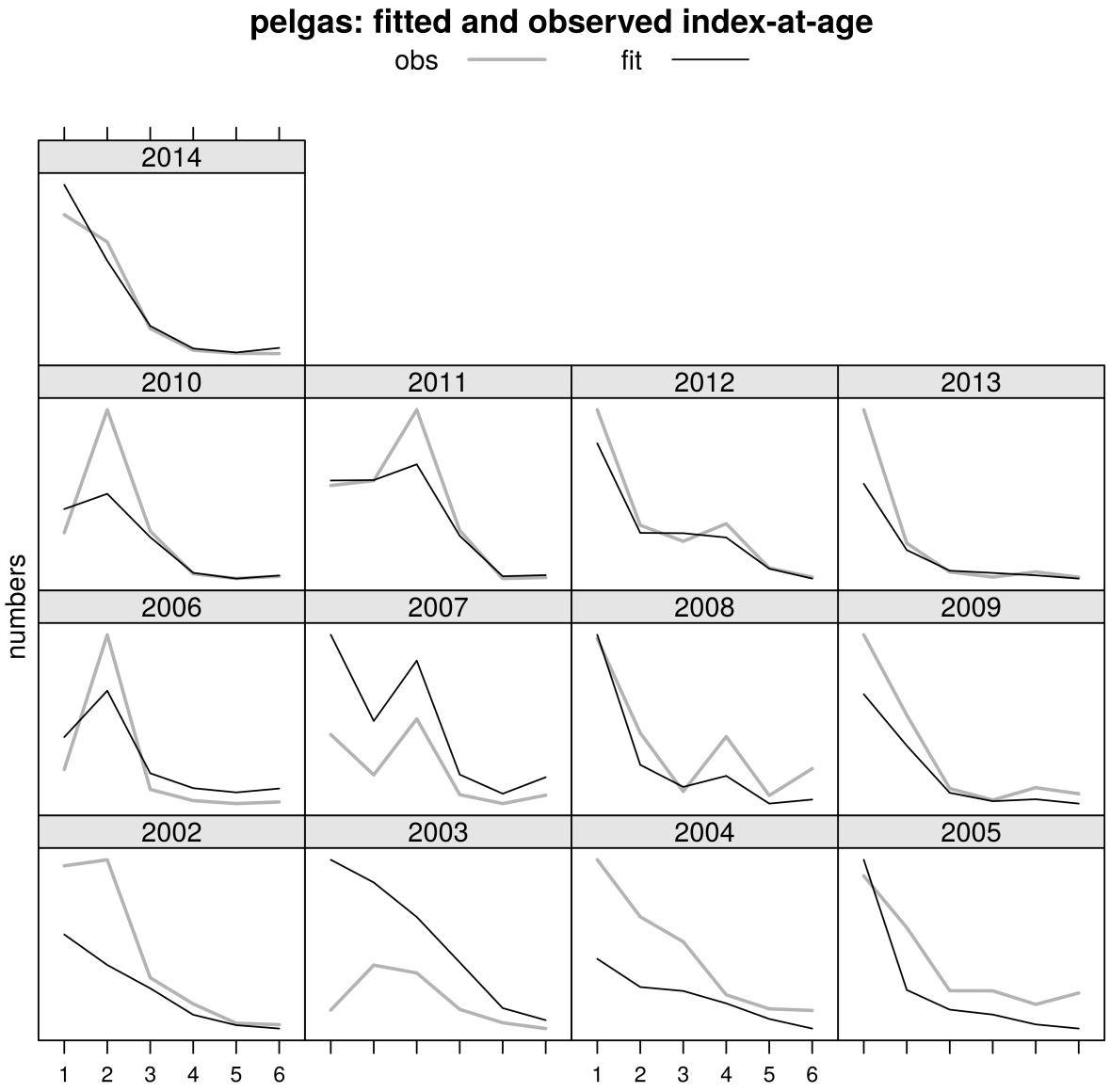

Figure 60: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(BB.q3f))
```

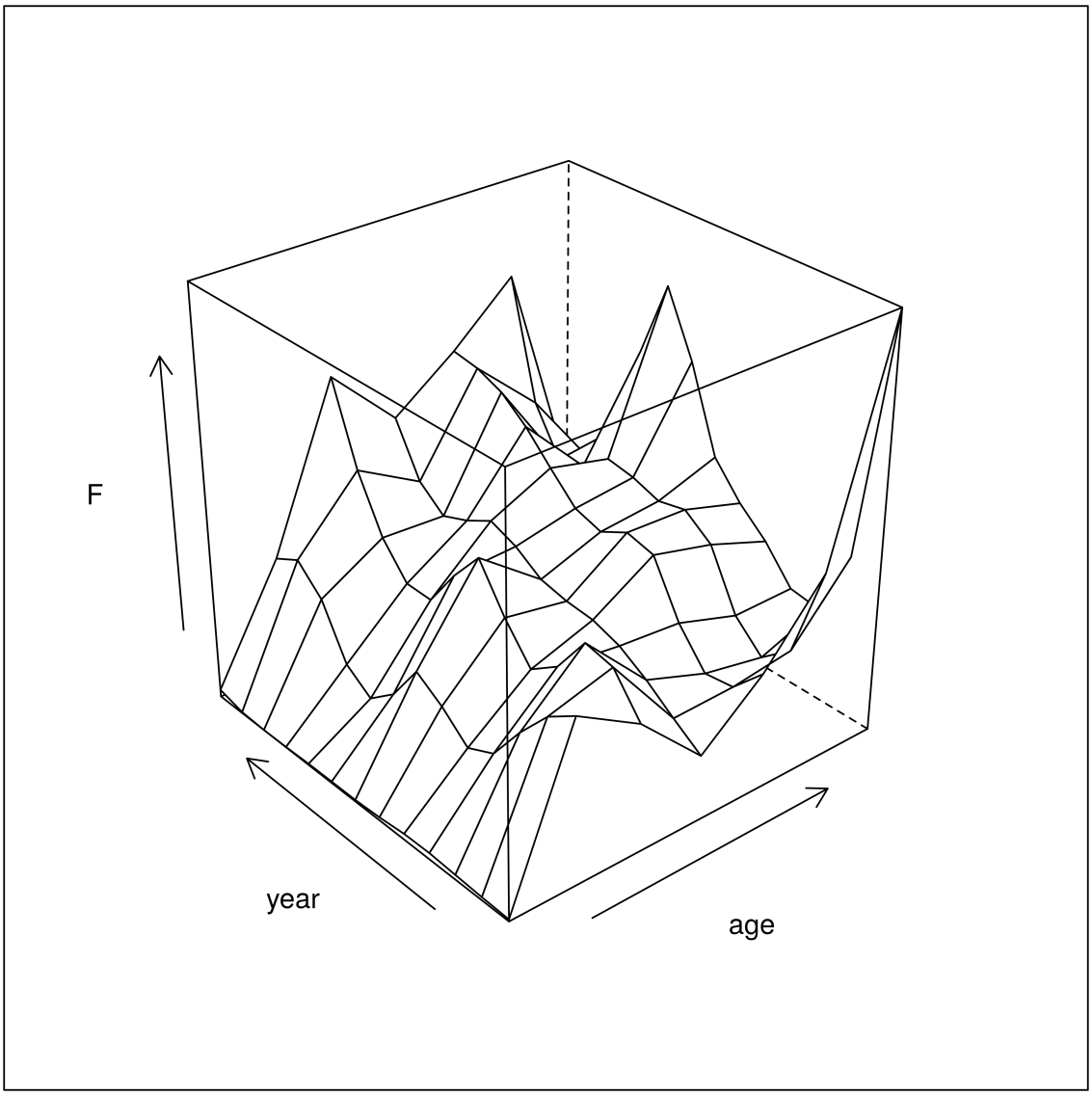

Figure 61: F-at-age estimate

```
plot(BB.q3mc)
```

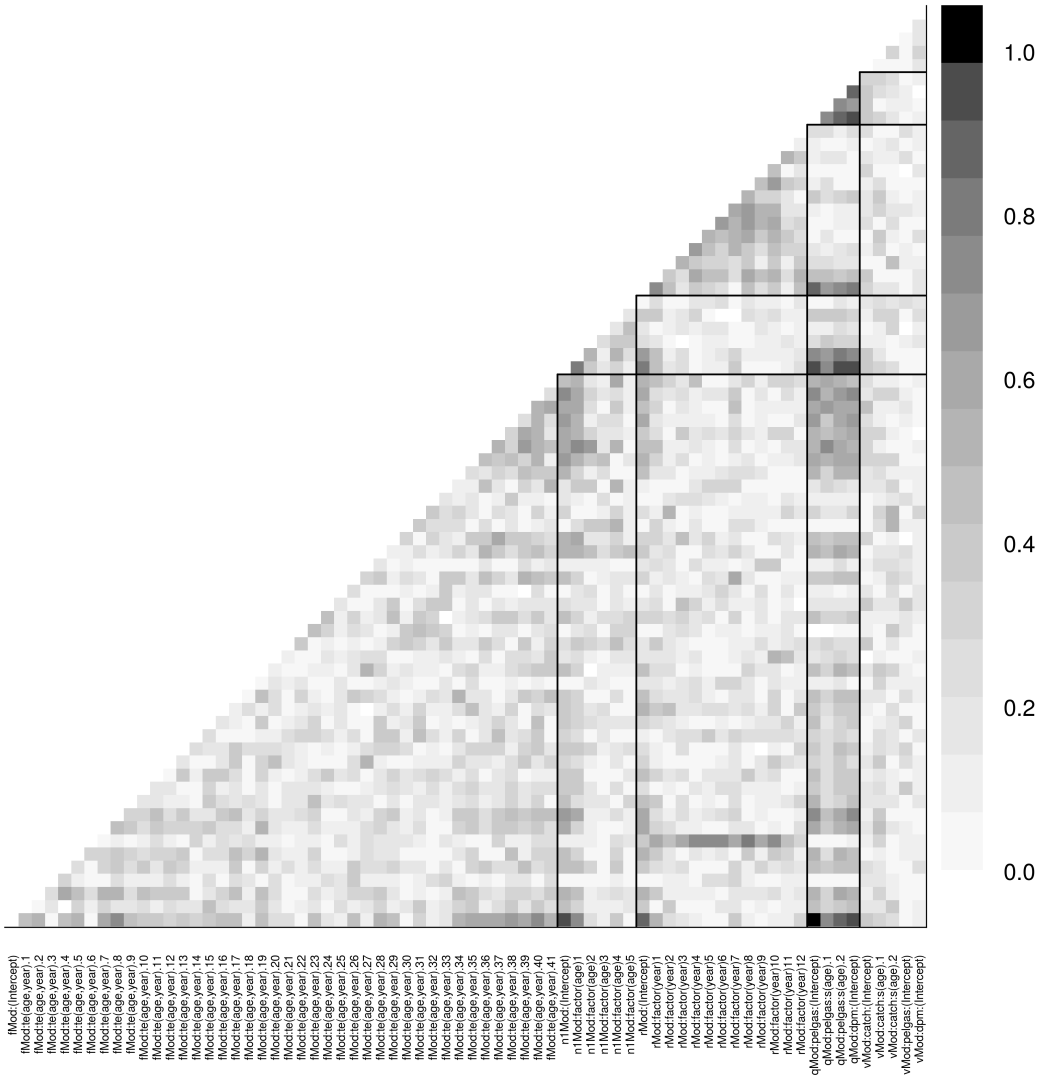

Figure 62: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(BB.q3smc)
```

Figure 63: Summary plot

5.4.4 q option 4: constant, survey overweighting

```
fmod <- ~te(age, year, k = c(6, 7))
qmod <- list(~1, ~1)
BB.idx2 <- BB.idx
index.var(BB.idx2[[1]]) <- 0.5
BB.q4f <- a4aSCA(BB.stk, BB.idx2, fmodel = fmod, qmodel = qmod)
BB.q4r <- residuals(BB.q4f, BB.stk, BB.idx2)
BB.q4s <- BB.stk + simulate(BB.q4f, 500)
BB.q4mc <- a4aSCA(BB.stk, BB.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
BB.q4mcmc <- as.mcmc(BB.q4mc)
BB.q4smc <- BB.stk + BB.q4mc
```

```
plot(BB.q4r)
```

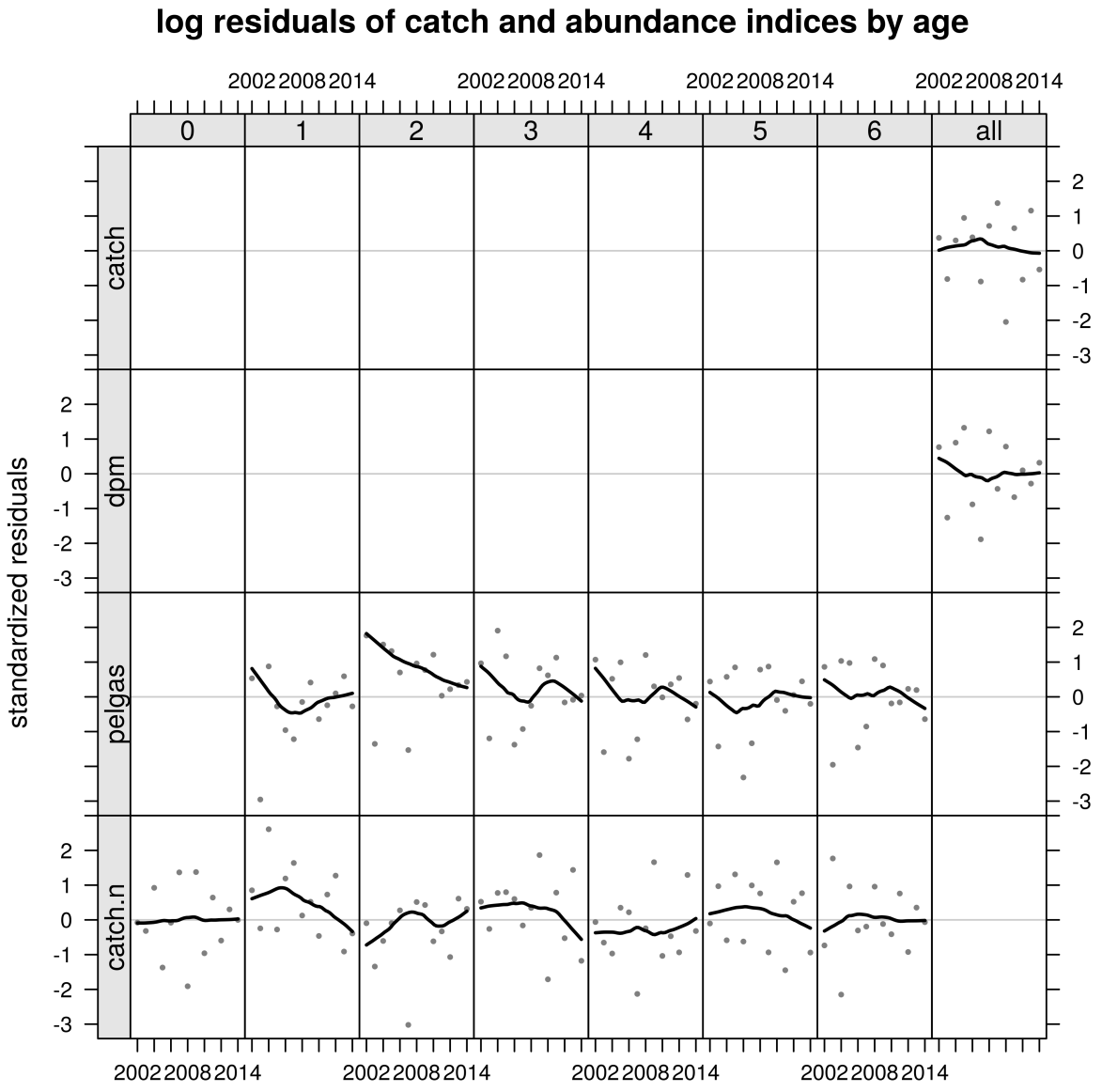

Figure 64: Residuals

```
plot(BB.q4f, BB.stk)
```

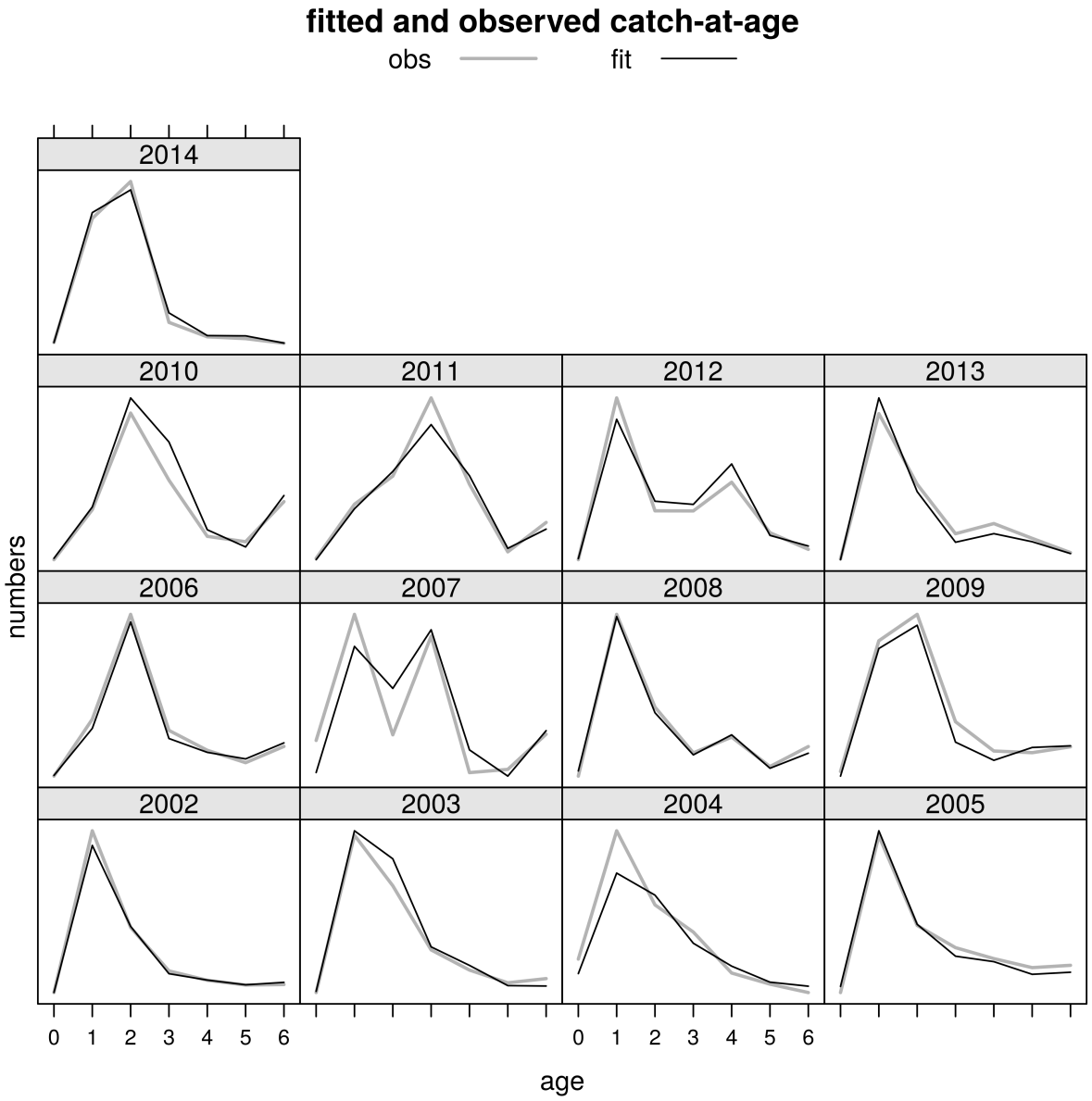

Figure 65: Catch-at-age predictions and observations

```
plot(BB.q4f, BB.idx2[1])
```

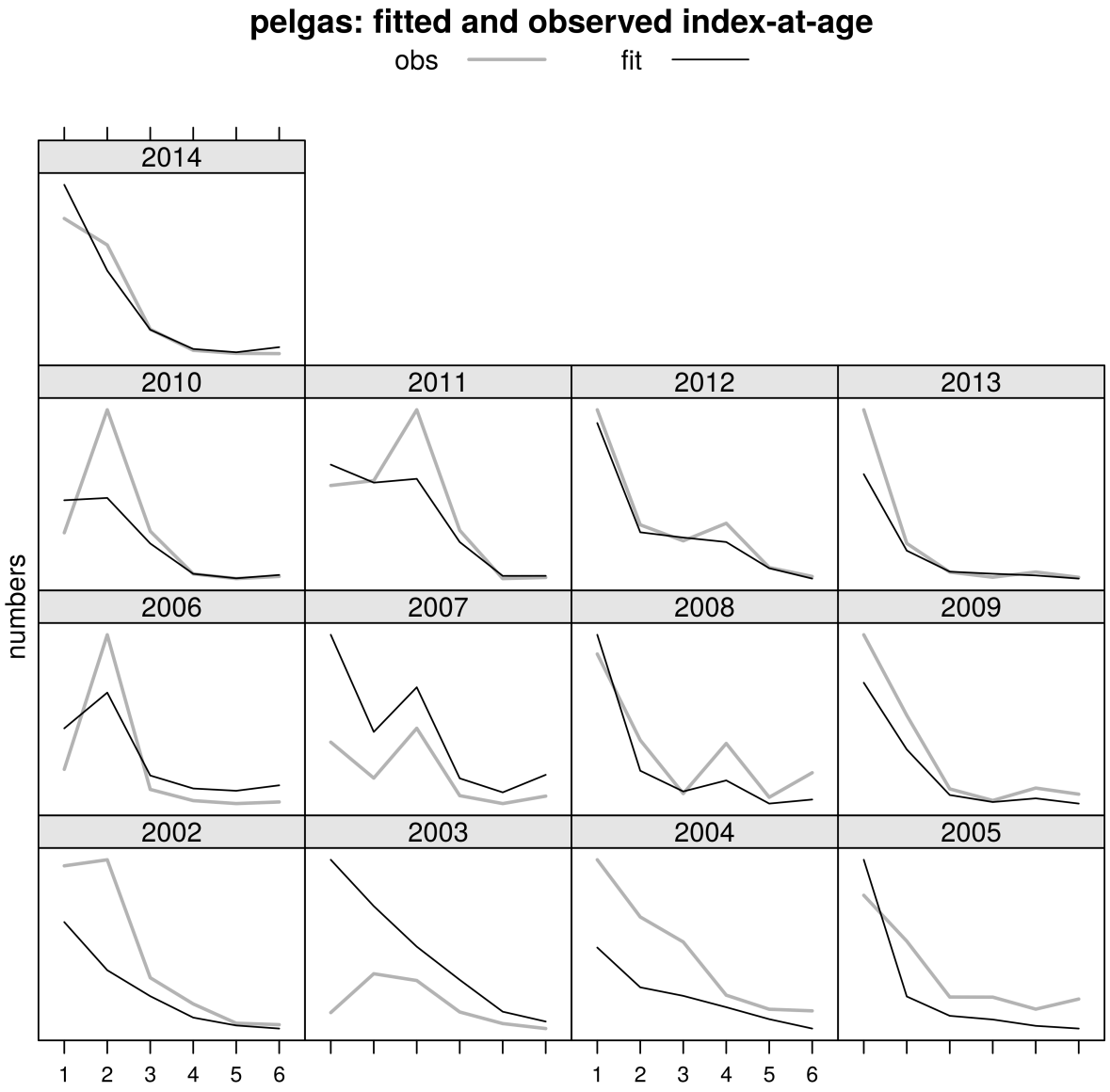

Figure 66: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(BB.q4f))
```

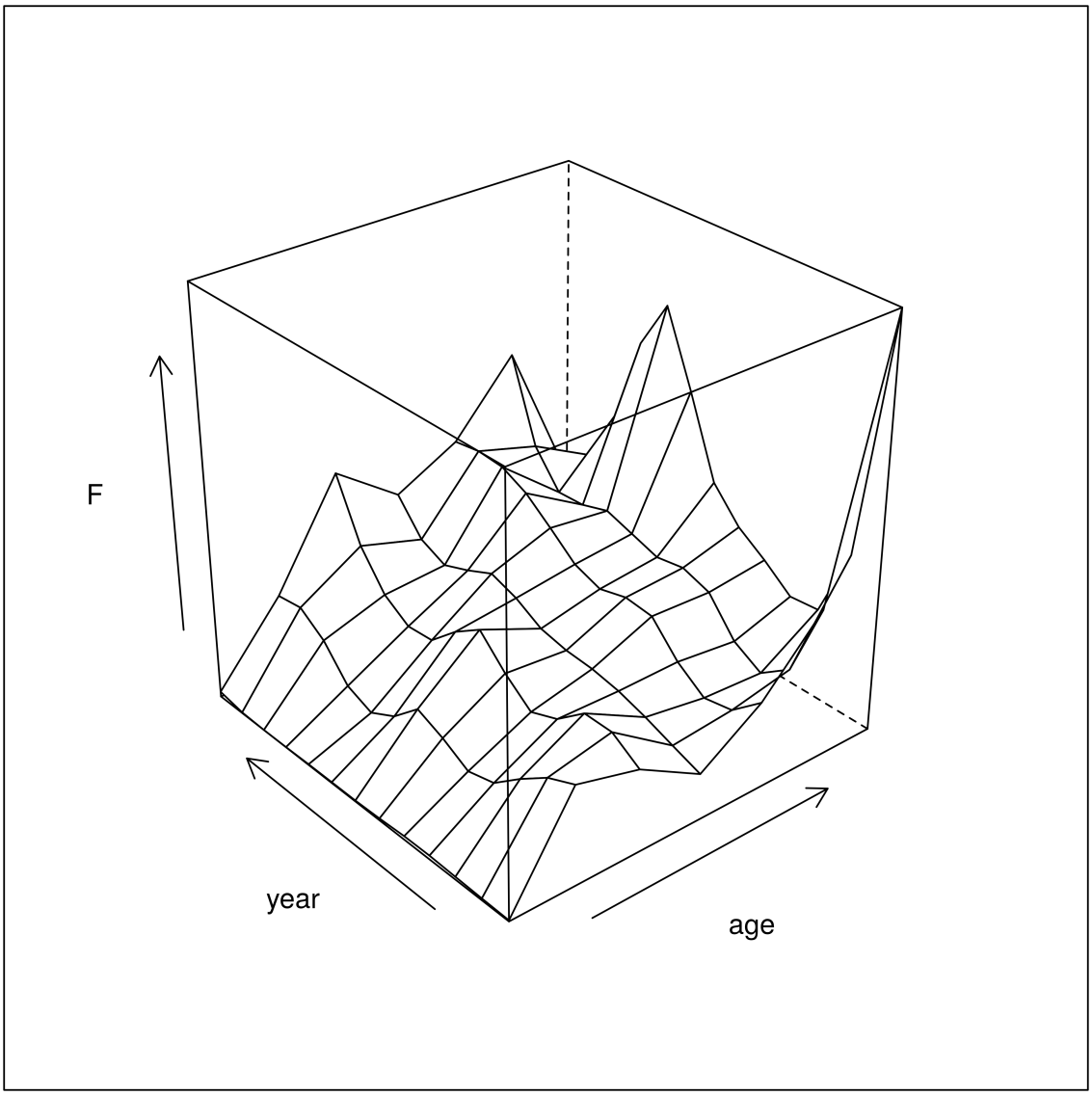

Figure 67: F-at-age estimate

```
plot(BB.q4mc)
```

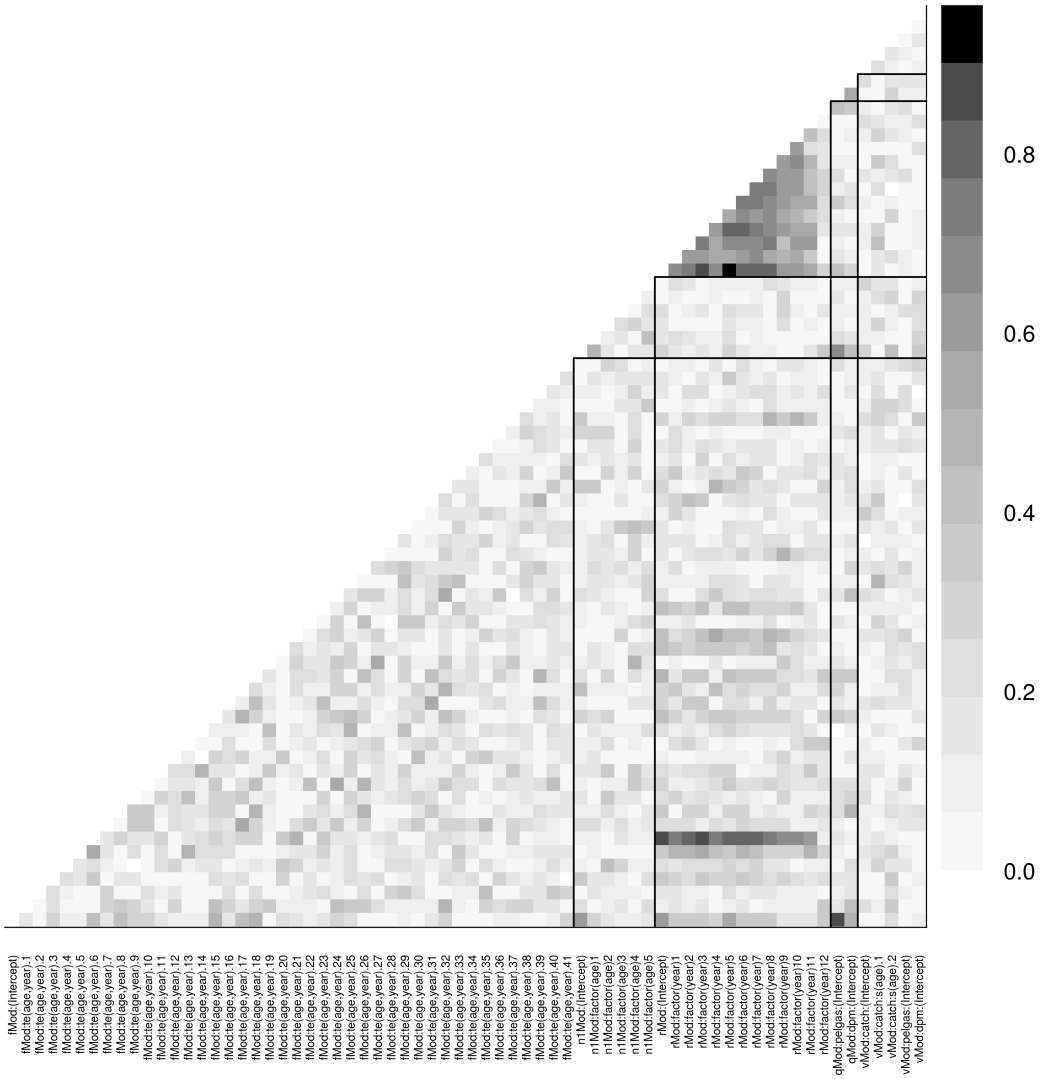

Figure 68: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(BB.q4smc)
```

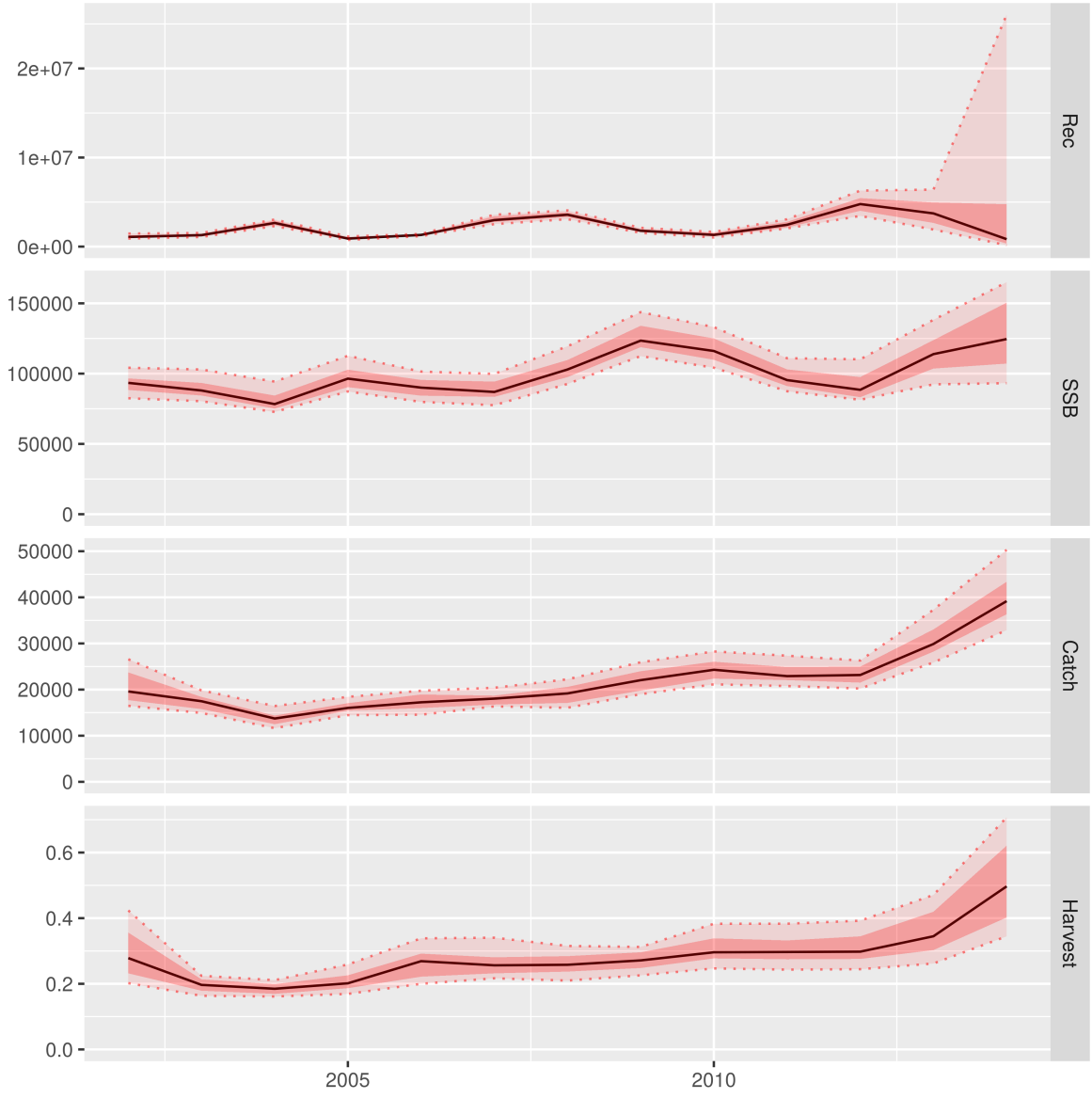

Figure 69: Summary plot

5.4.5 q option 5: constant, no overweighting of survey, no DEPM

```
fmod <- ~te(age, year, k = c(6, 7))
qmod <- list(~1)
BB.q5f <- a4aSCA(BB.stk, BB.idx[1], fmodel = fmod, qmodel = qmod)
BB.q5r <- residuals(BB.q5f, BB.stk, BB.idx[1])
BB.q5s <- BB.stk + simulate(BB.q5f, 500)
BB.q5mc <- a4aSCA(BB.stk, BB.idx[1], fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
BB.q5mcmc <- as.mcmc(BB.q5mc)
BB.q5smc <- BB.stk + BB.q5mc
```

```
plot(BB.q5r)
```

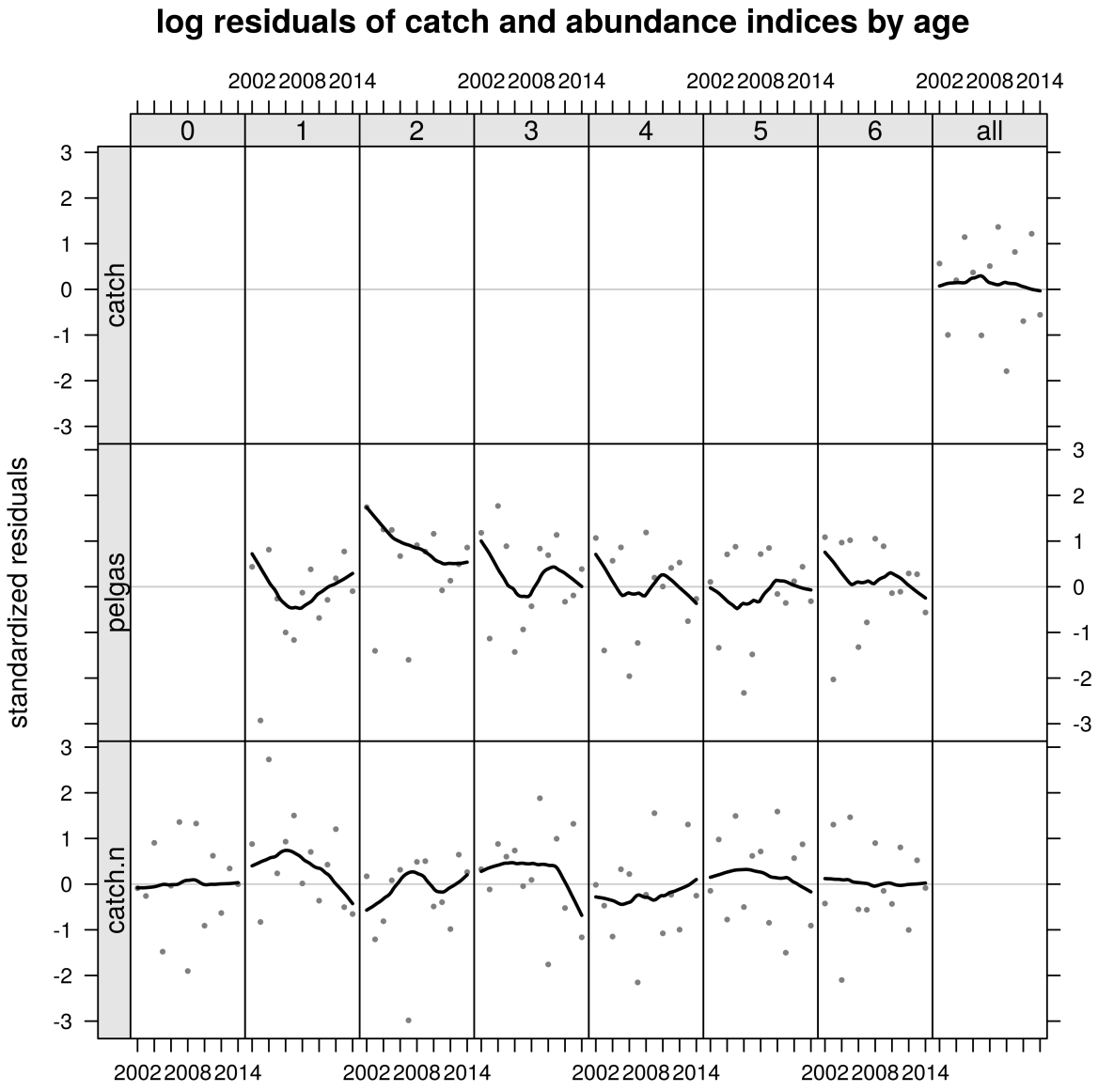

Figure 70: Residuals

```
plot(BB.q5f, BB.stk)
```

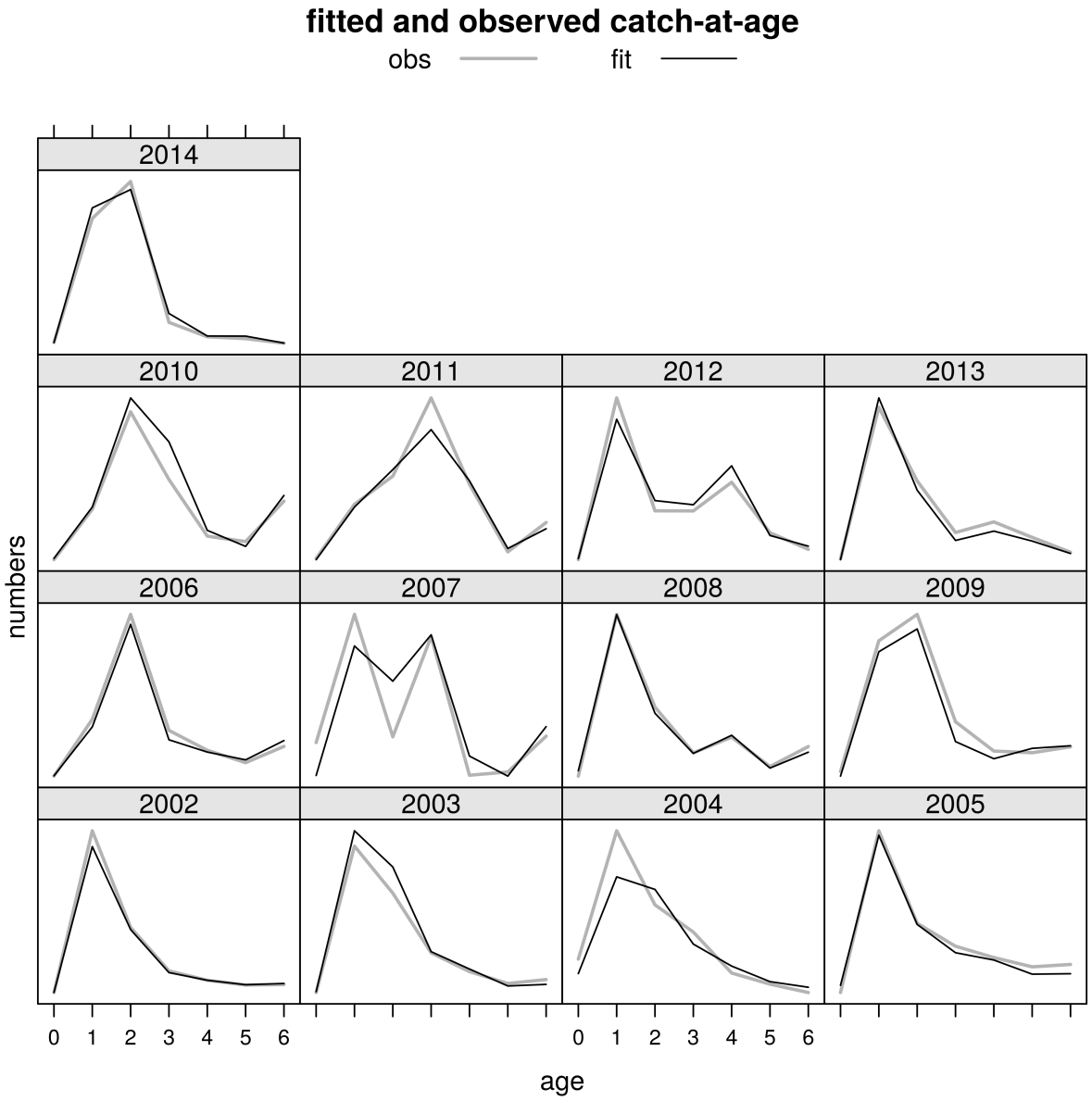

Figure 71: Catch-at-age predictions and observations

```
plot(BB.q5f, BB.idx[1])
```

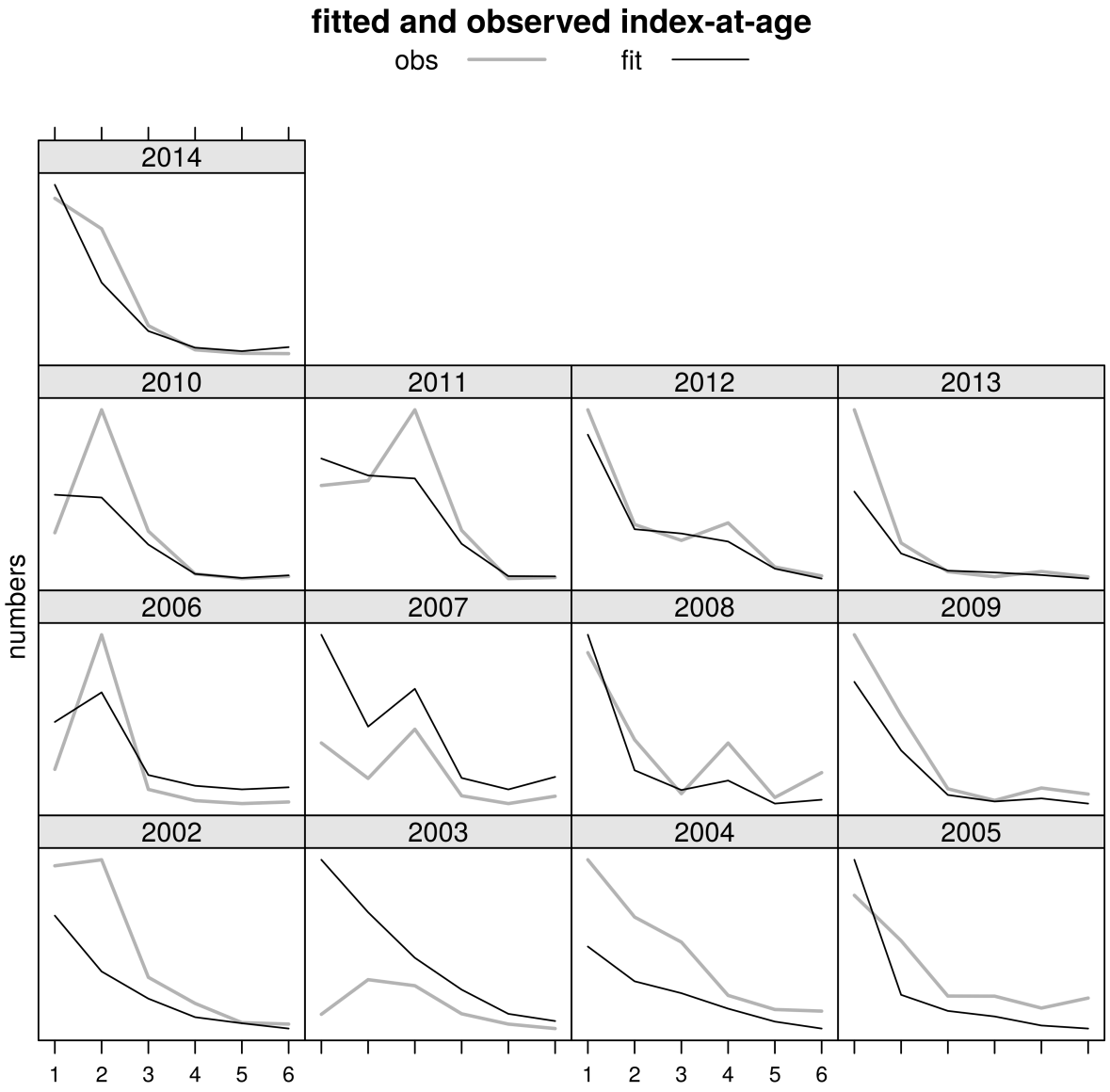

Figure 72: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(BB.q5f))
```

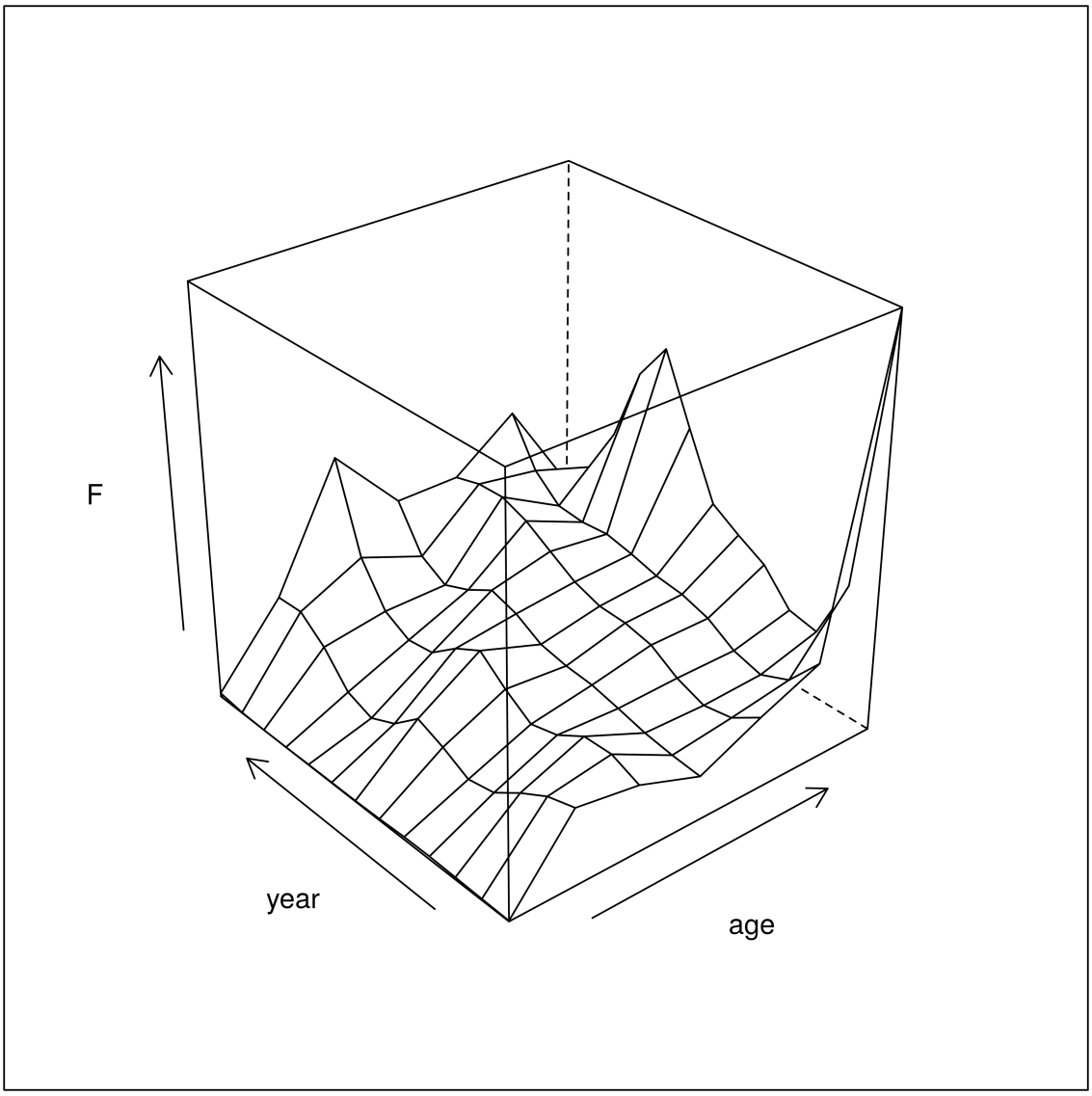

Figure 73: F-at-age estimate

```
plot(BB.q5mc)
```

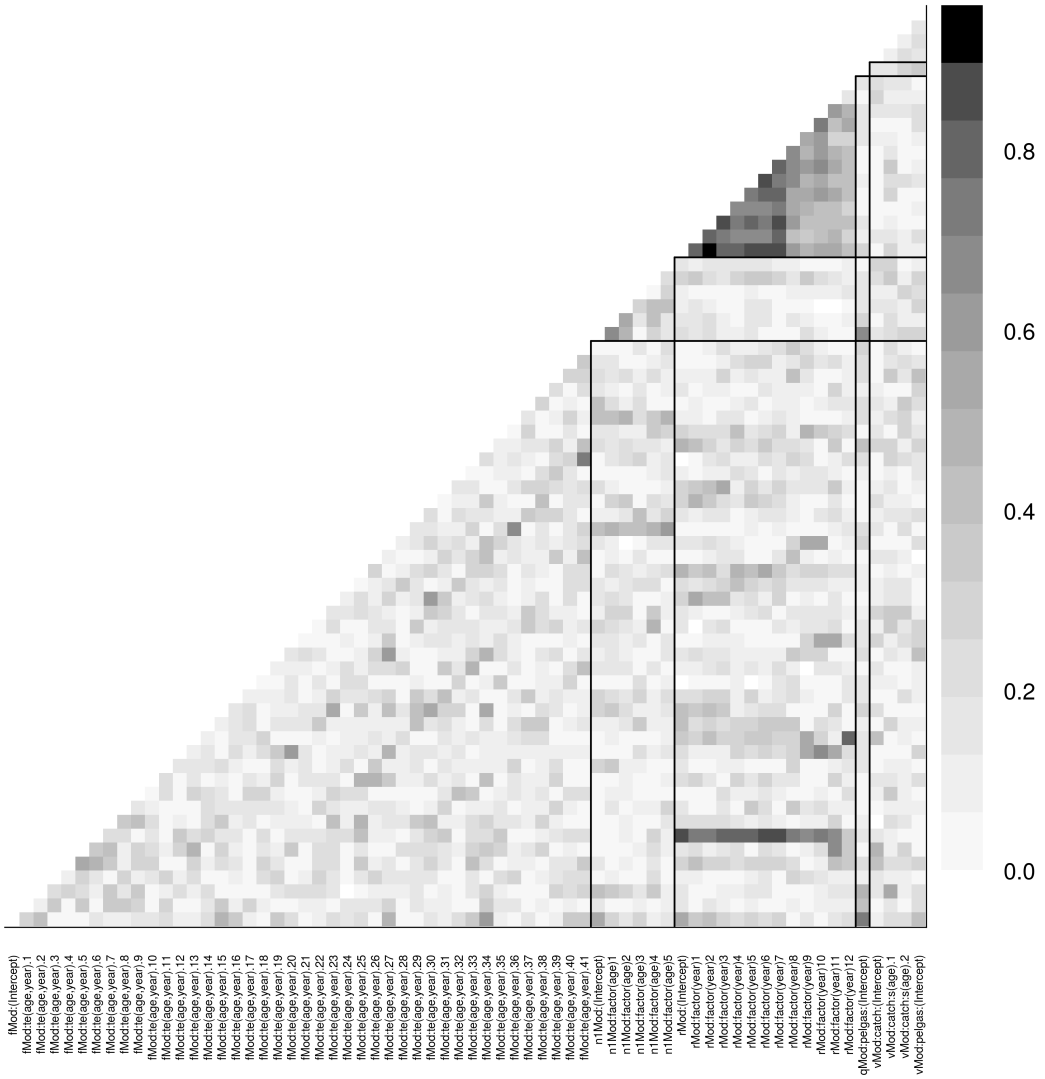

Figure 74: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(BB.q5smc)
```

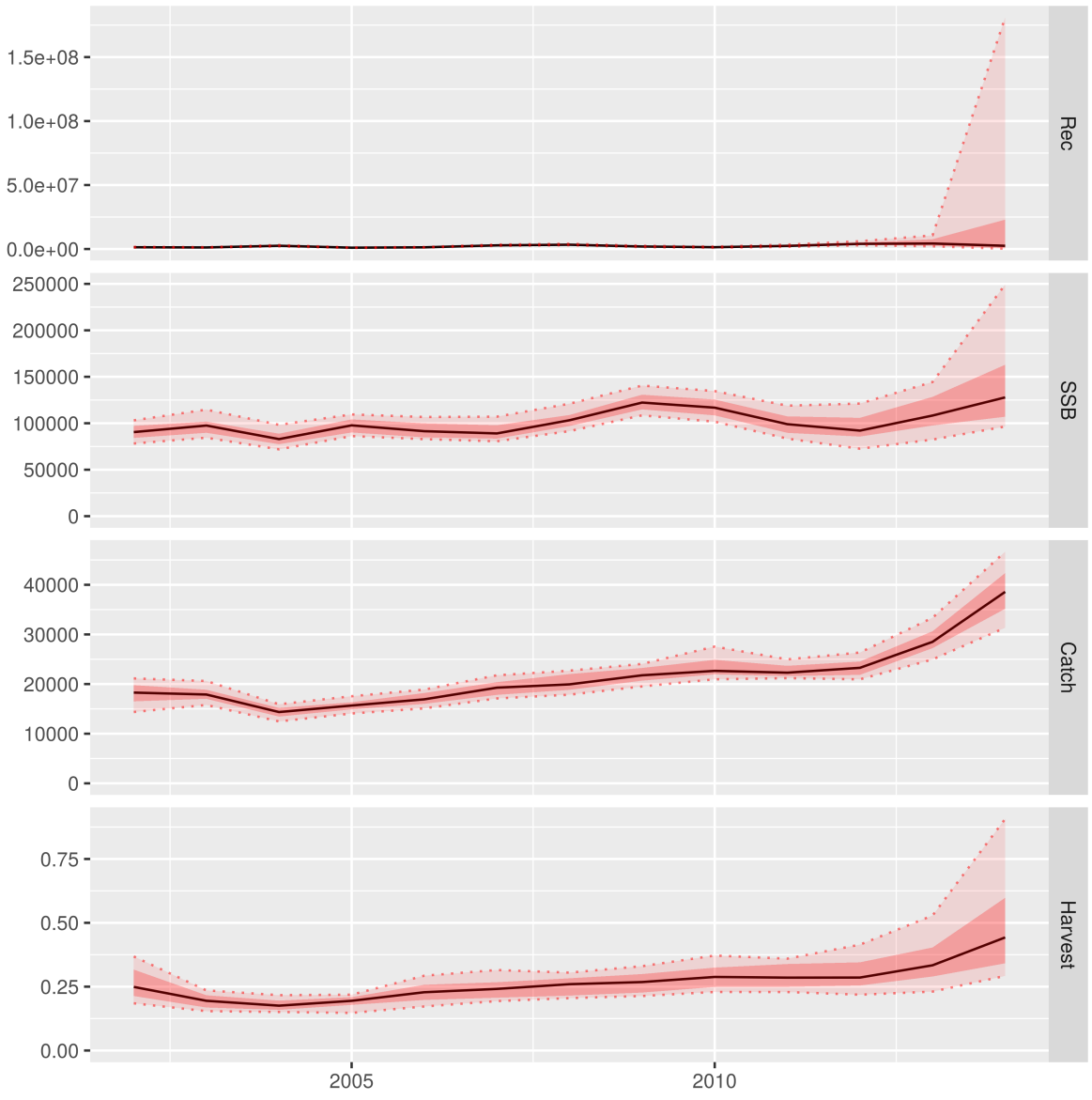

Figure 75: Summary plot

5.4.6 Comparison across assessments

```
plot(FLStocks(q1 = BB.q1smc, q2 = BB.q2smc, q3 = BB.q3smc, q4 = BB.q4smc,
    q5 = BB.q5smc))
```

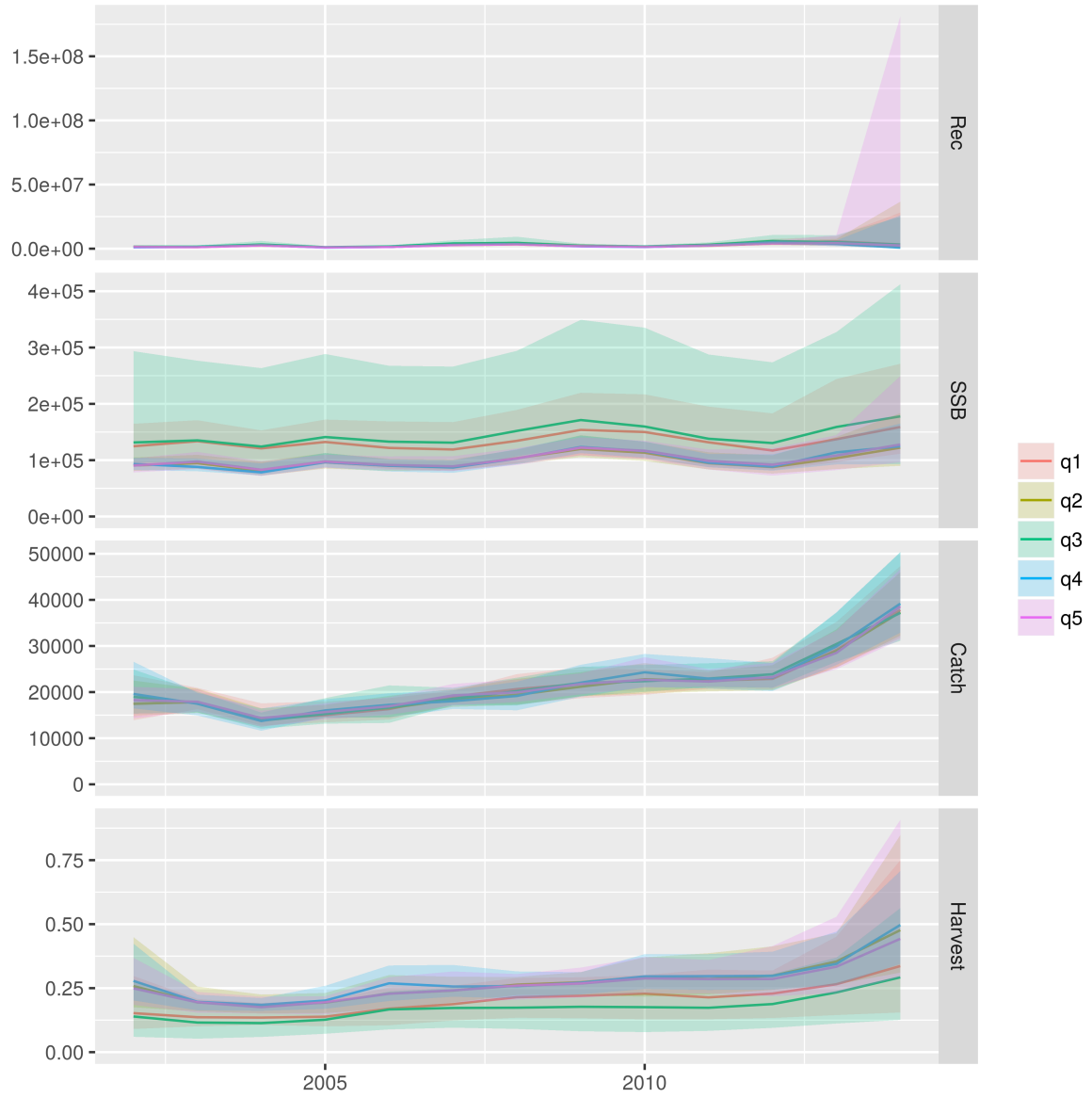

Figure 76: All assessments summary

5.5 The Northwestern sub-unit

```
load("../analysis/NW/NW.Rdata")
index(NW.idx[[1]])[, 9] <- NA
index(NW.idx[[1]])[, 17] <- NA
```

5.5.1 q option 1: smoother, no overweighting of survey

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 12))
qmod <- list(~s(age, k = 5), ~1)
NW.q1f <- a4aSCA(NW.stk, NW.idx, fmodel = fmod, qmodel = qmod)
NW.q1r <- residuals(NW.q1f, NW.stk, NW.idx)
NW.q1s <- NW.stk + simulate(NW.q1f, 500)
NW.q1mc <- a4aSCA(NW.stk, NW.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
NW.q1mcmc <- as.mcmc(NW.q1mc)
NW.q1smc <- NW.stk + NW.q1mc
```

```
plot(NW.q1r)
```

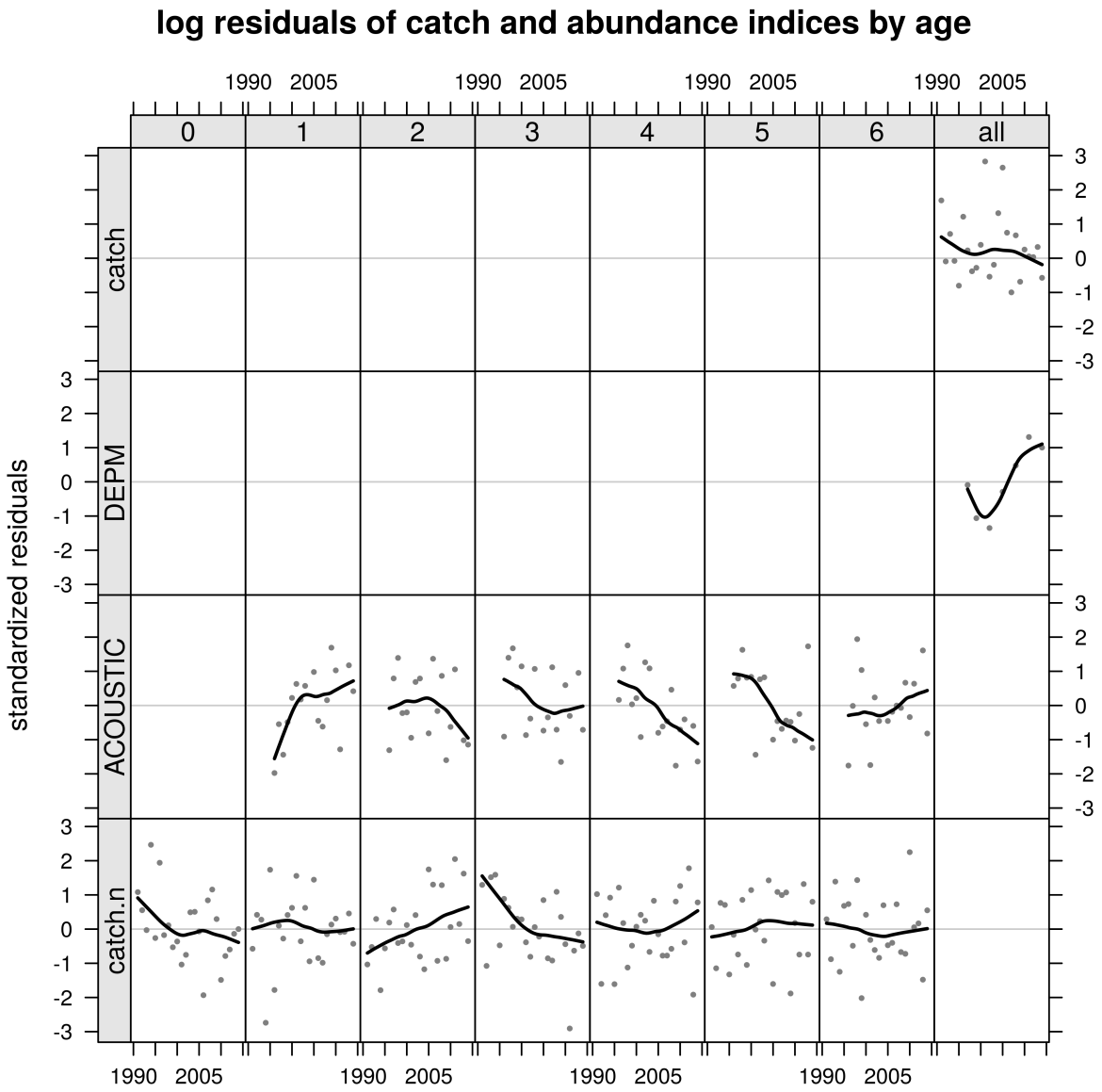

Figure 77: Residuals

```
plot(NW.q1f, NW.stk)
```

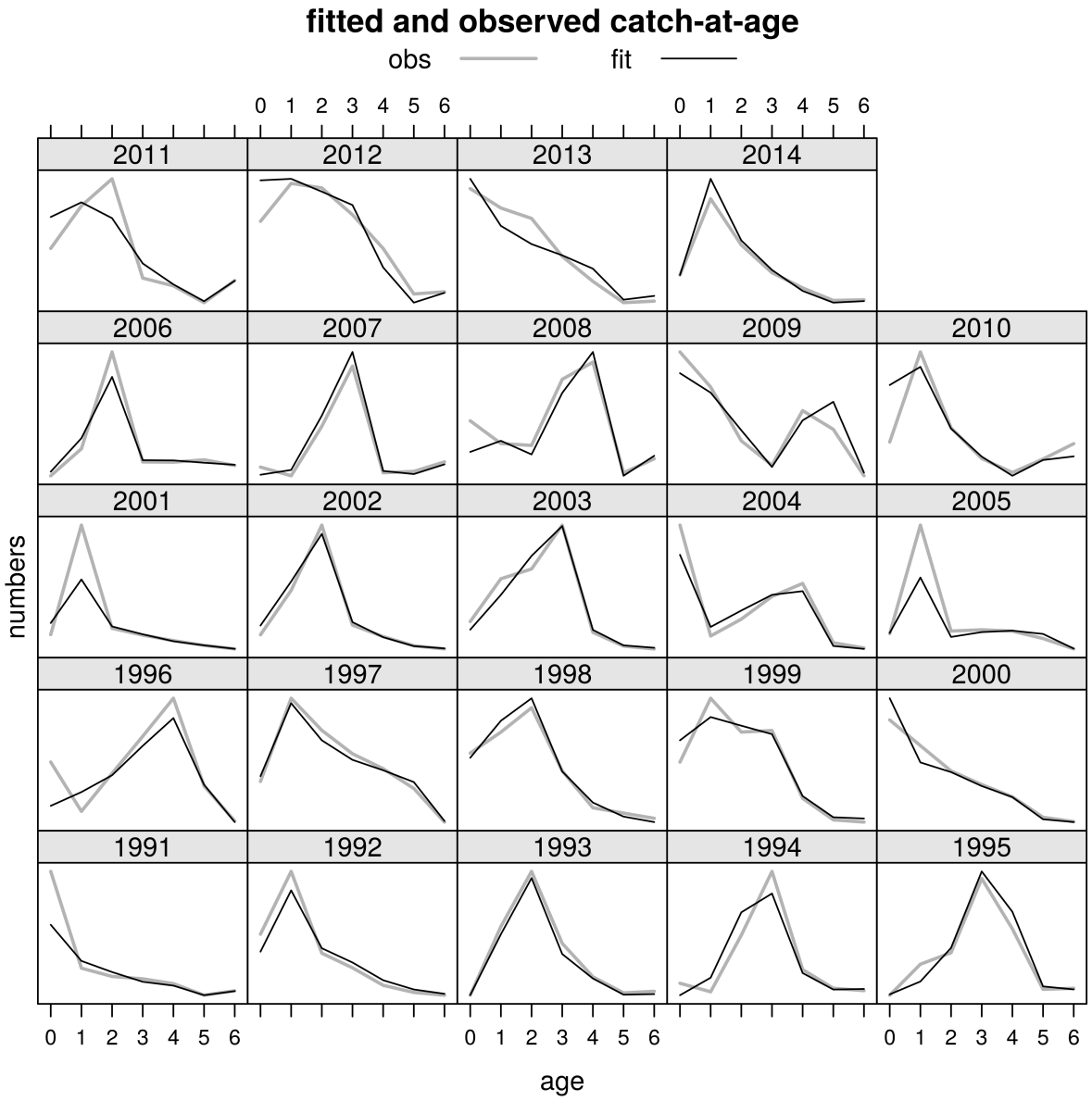

Figure 78: Catch-at-age predictions and observations

```
plot(NW.q1f, NW.idx[1])
```

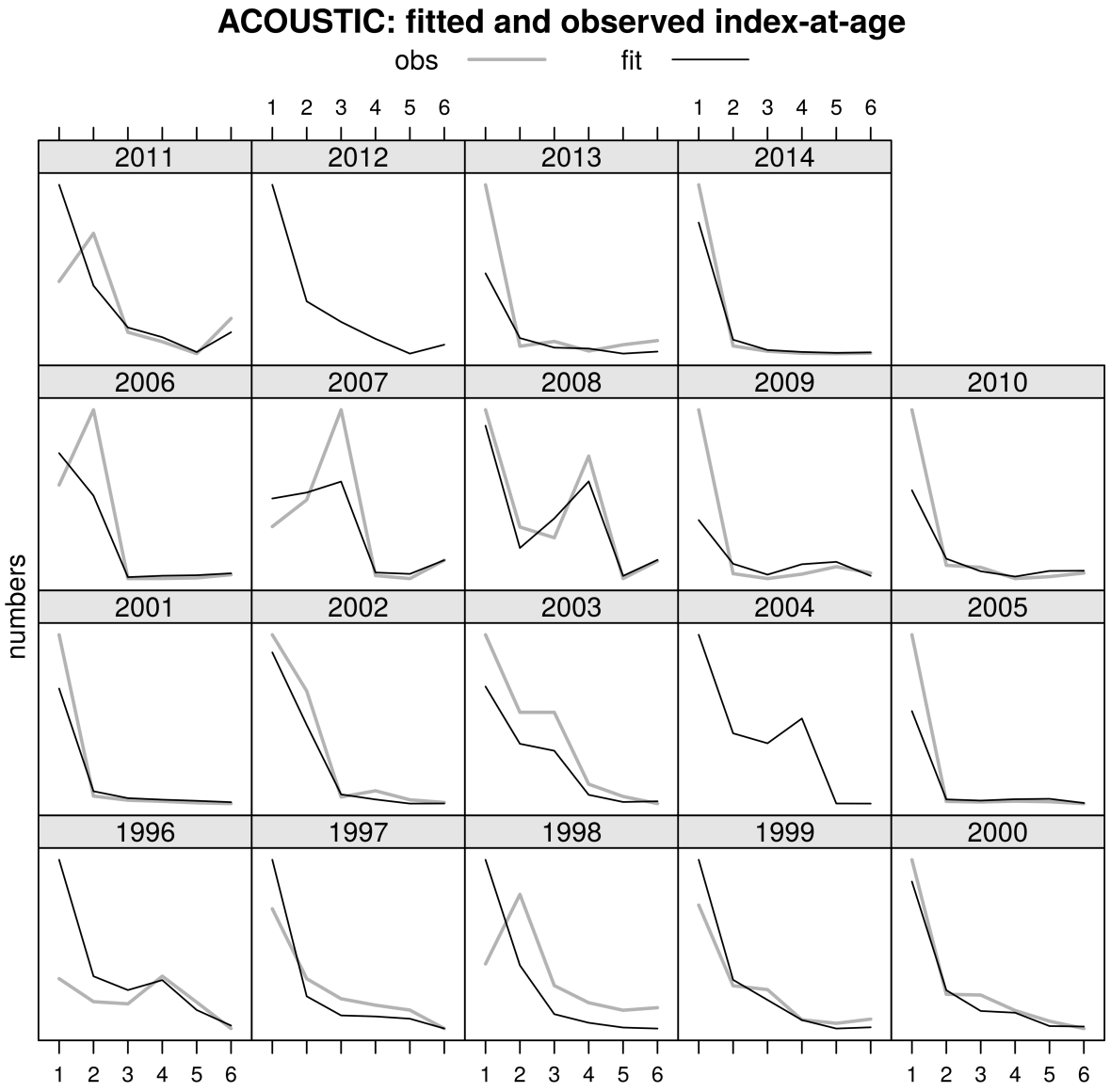

Figure 79: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(NW.q1f))
```

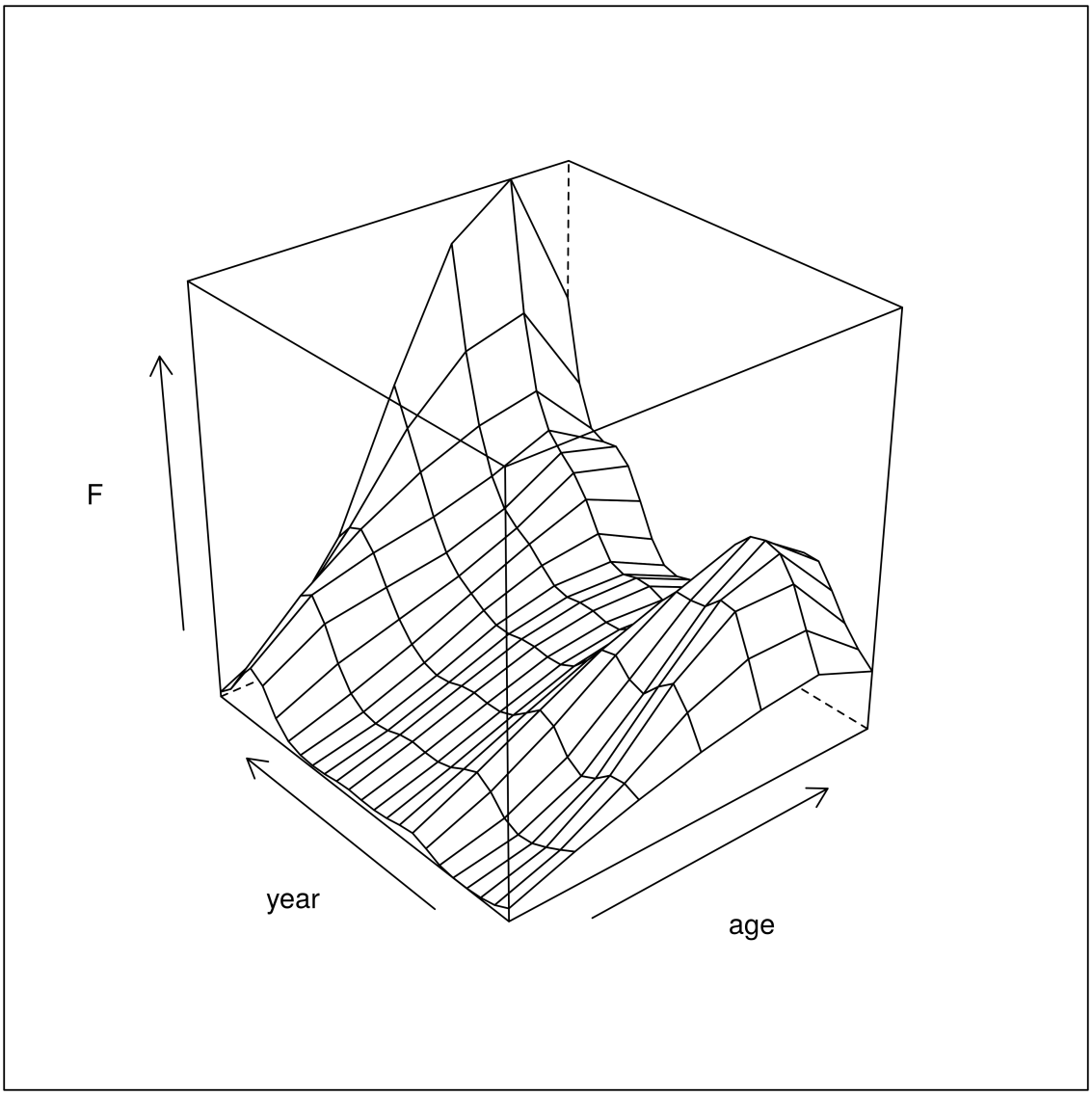

Figure 80: F-at-age estimate

```
plot(NW.q1mc)
```

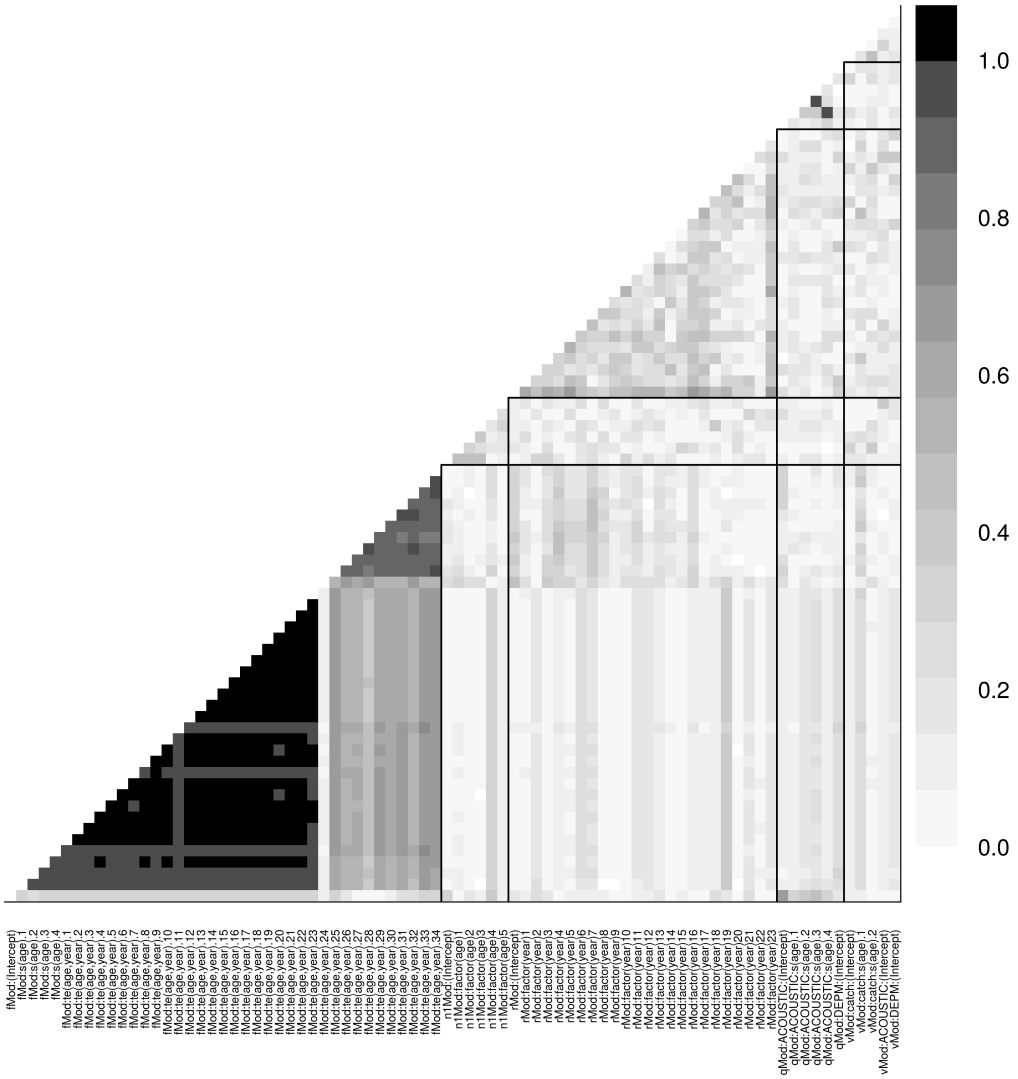

Figure 81: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(NW.q1smc)
```

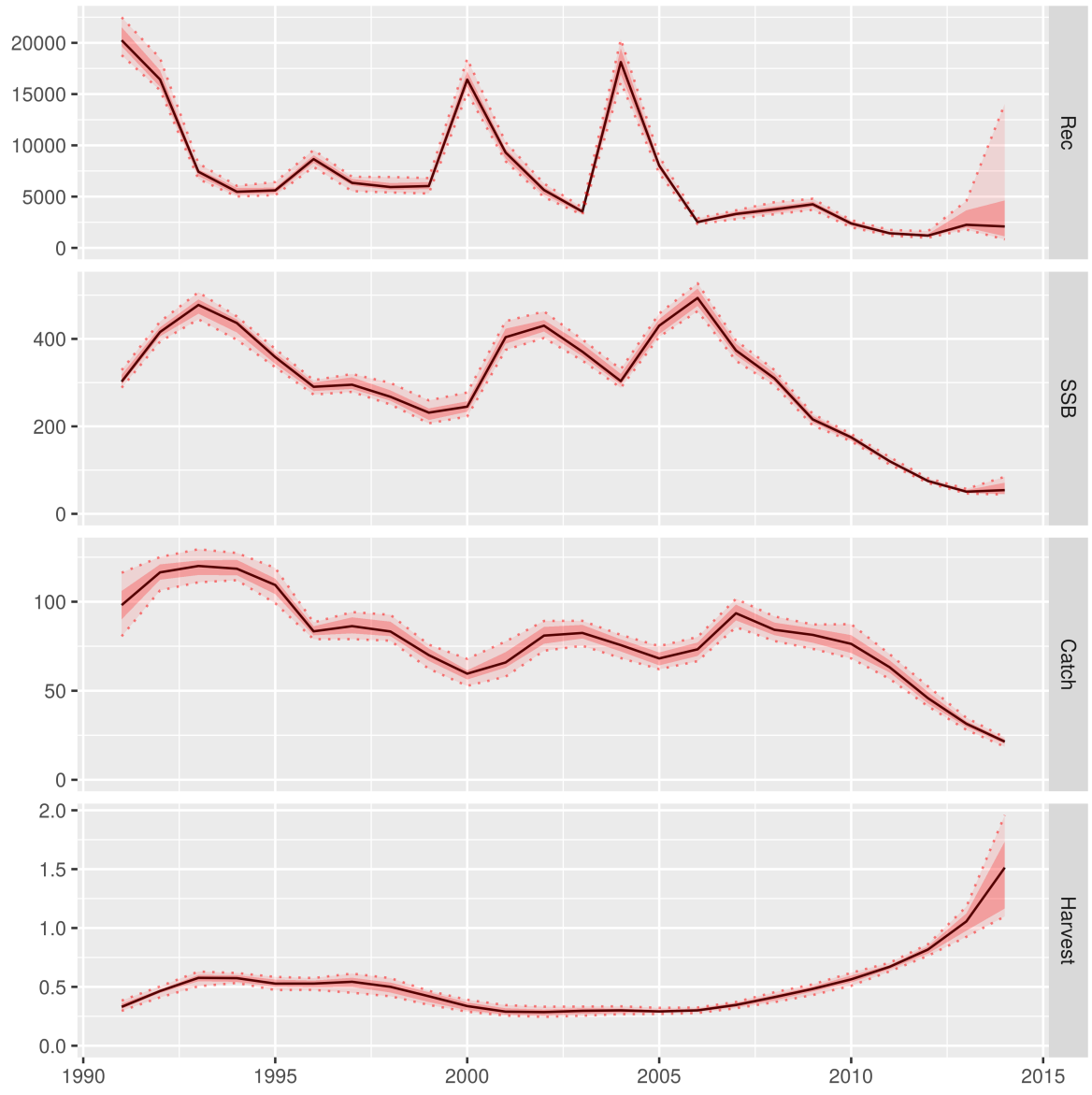

Figure 82: Summary plot

5.5.2 q option 2: constant, no overweighting of survey

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 12))
qmod <- list(~1, ~1)
NW.q2f <- a4aSCA(NW.stk, NW.idx, fmodel = fmod, qmodel = qmod)
NW.q2r <- residuals(NW.q2f, NW.stk, NW.idx)
NW.q2s <- NW.stk + simulate(NW.q2f, 500)
NW.q2mc <- a4aSCA(NW.stk, NW.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
NW.q2mcmc <- as.mcmc(NW.q2mc)
NW.q2smc <- NW.stk + NW.q2mc
```

```
plot(NW.q2r)
```

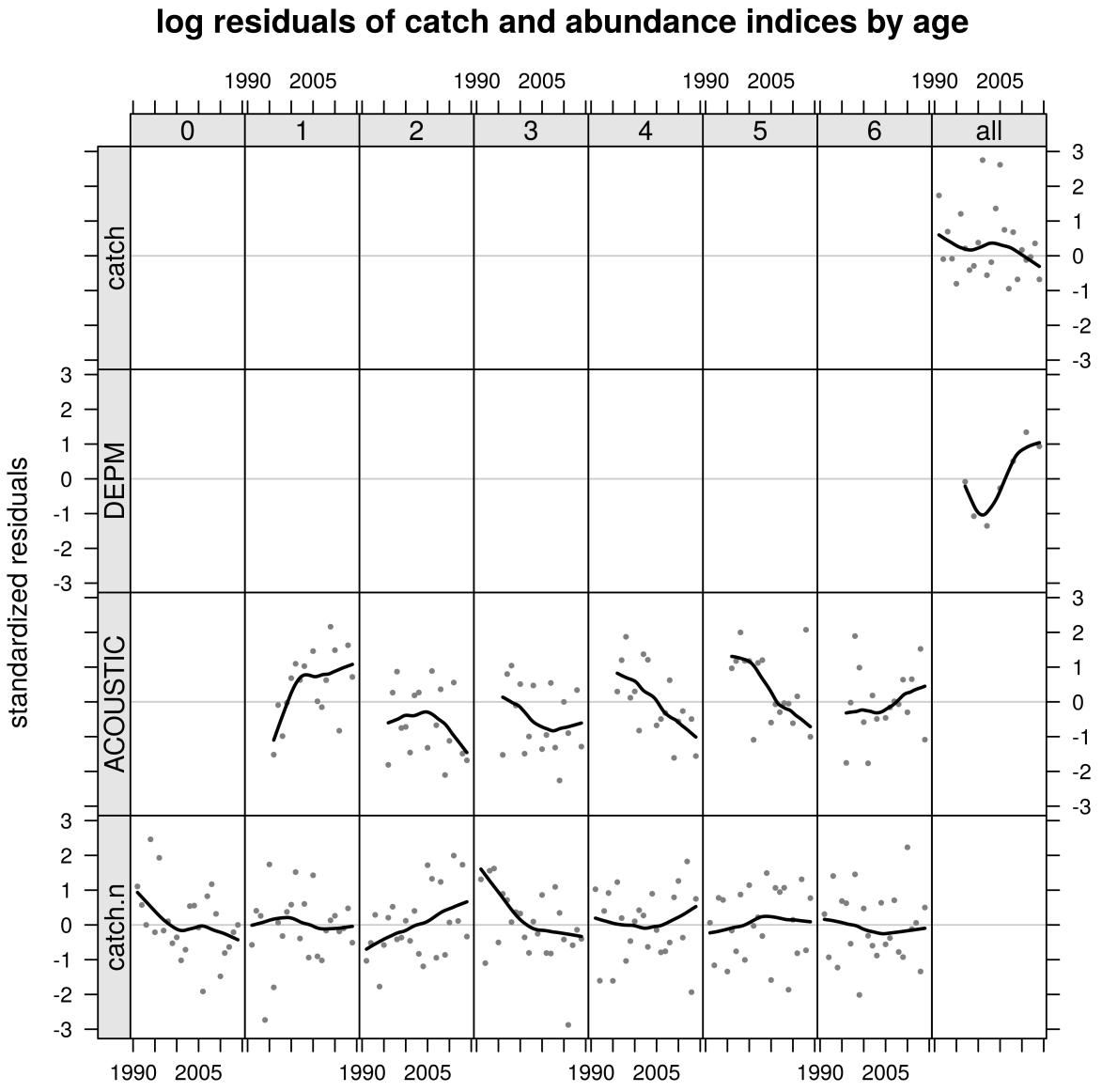

Figure 83: Residuals

```
plot(NW.q2f, NW.stk)
```

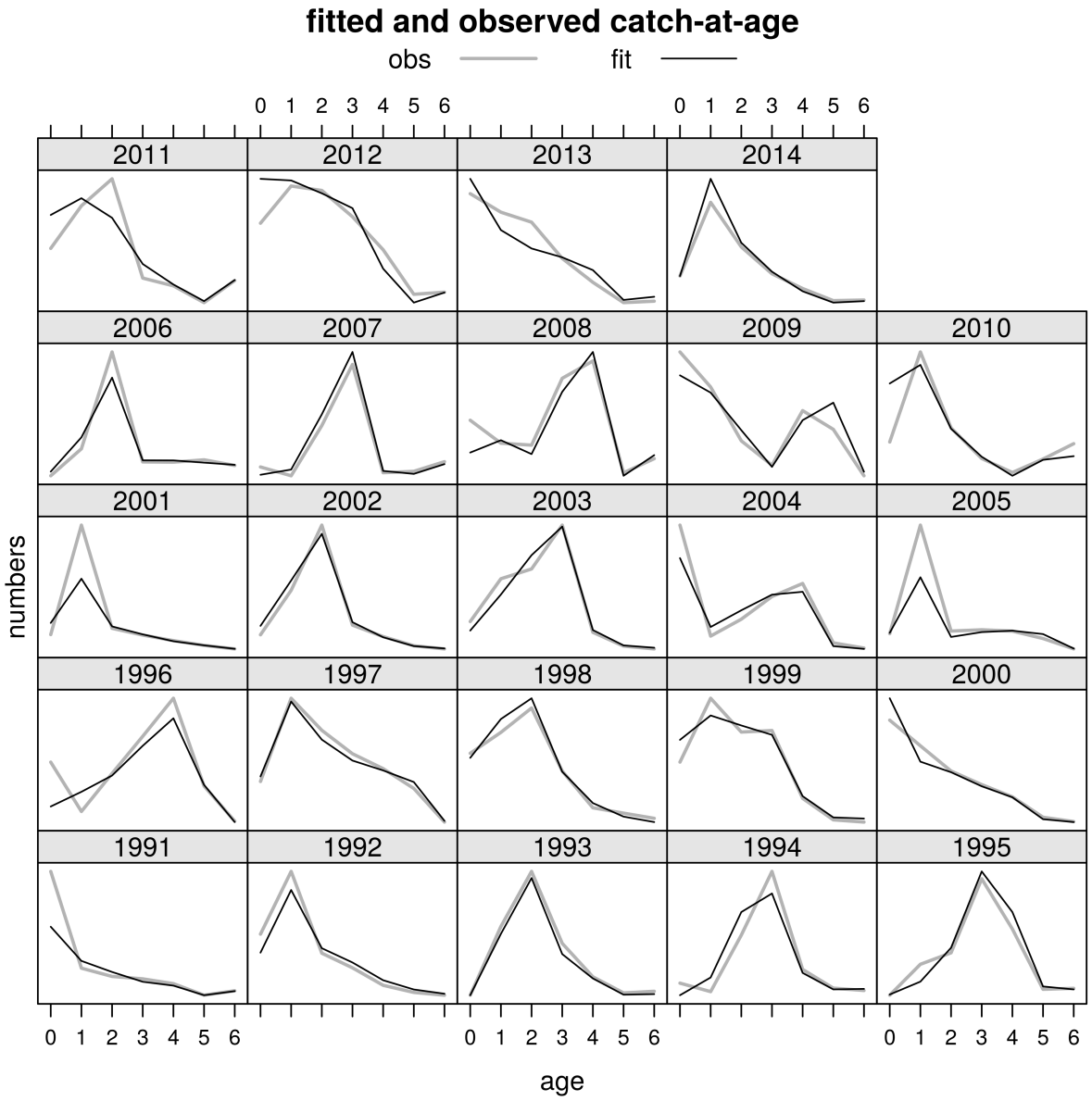

Figure 84: Catch-at-age predictions and observations

```
plot(NW.q2f, NW.idx[1])
```

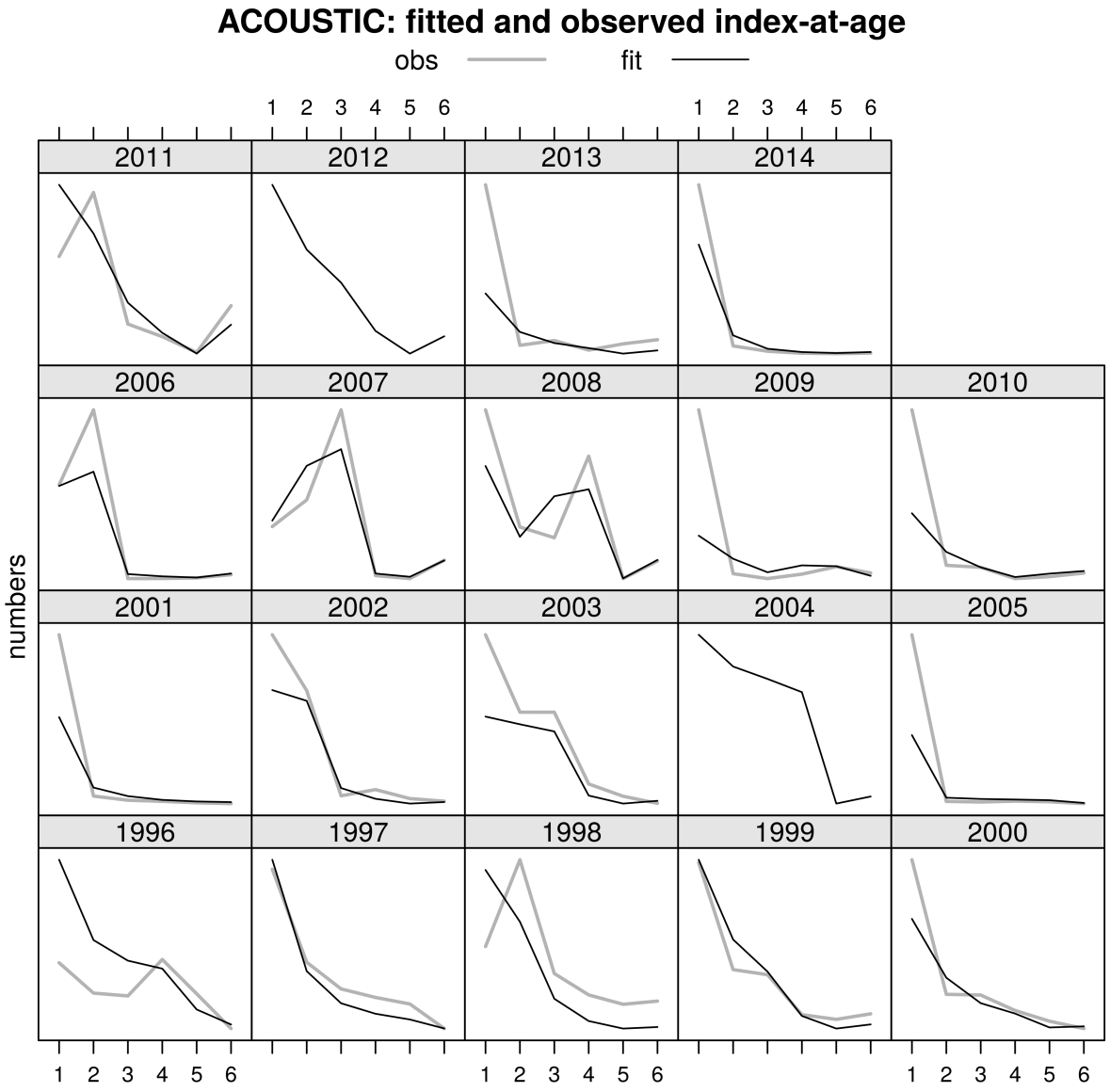

Figure 85: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(NW.q2f))
```

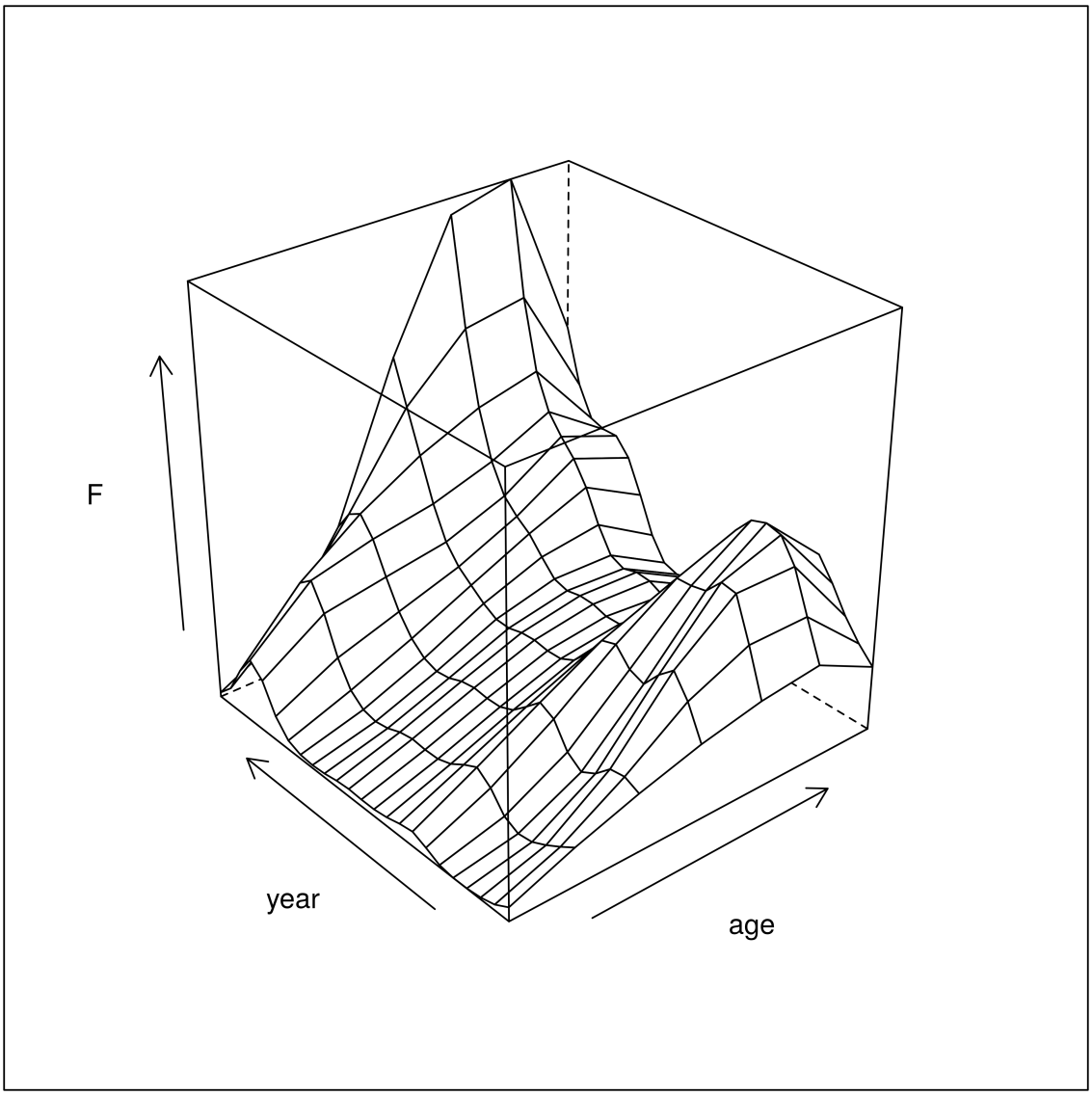

Figure 86: F-at-age estimate

```
plot(NW.q2mc)
```

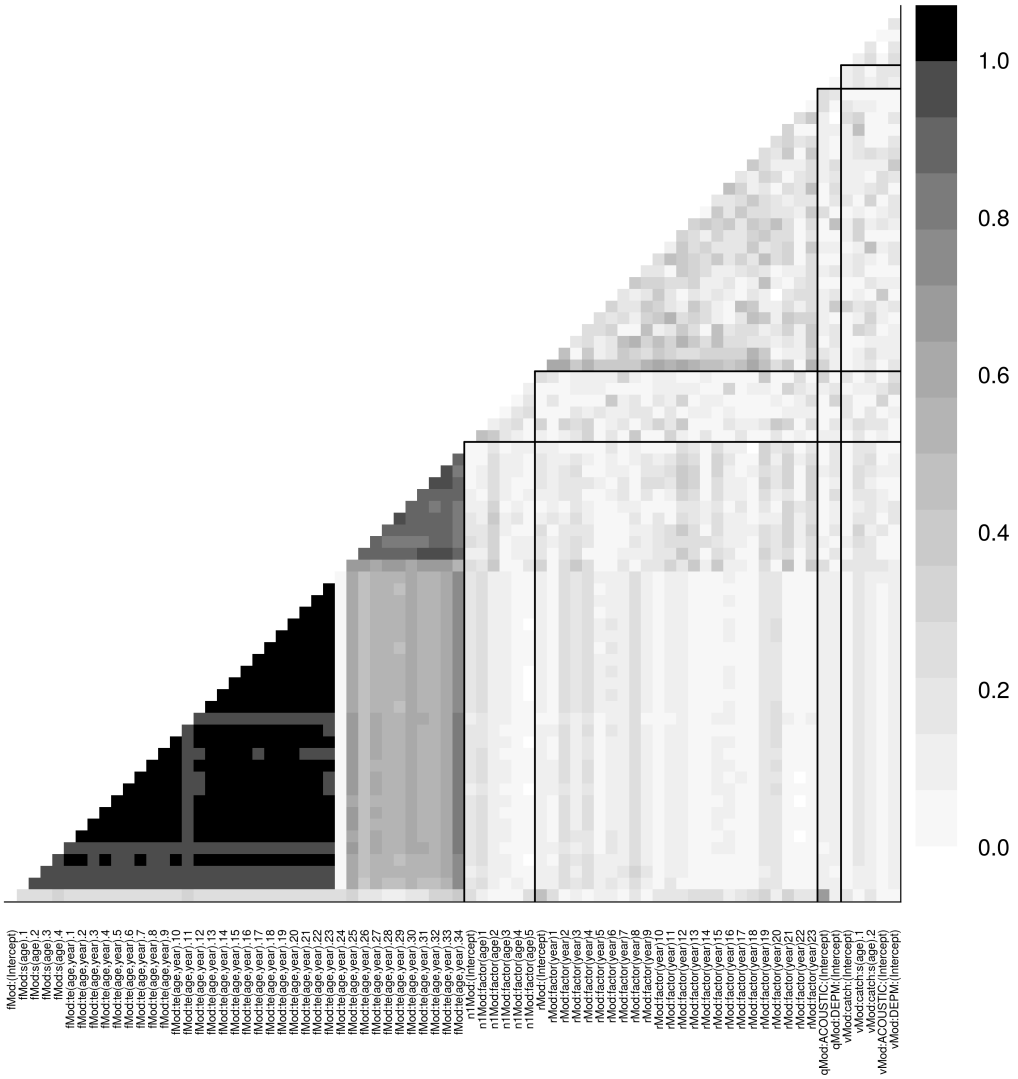

Figure 87: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(NW.q2smc)
```

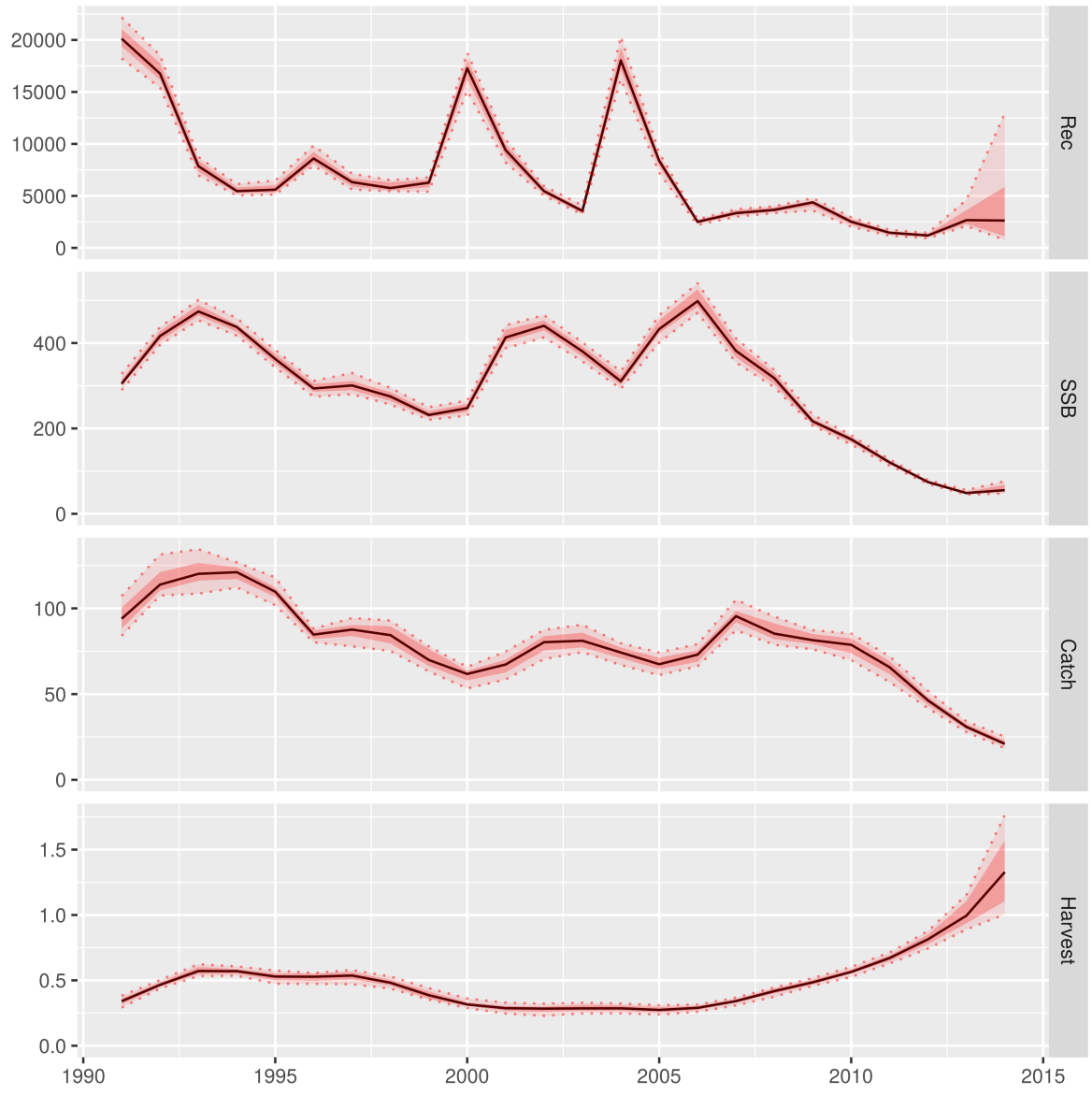

Figure 88: Summary plot

5.5.3 q option 3: smoother, survey overweighting

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 12))
qmod <- list(~s(age, k = 5), ~1)
NW.idx2 <- NW.idx
index.var(NW.idx2[[1]]) <- 0.5
NW.q3f <- a4aSCA(NW.stk, NW.idx2, fmodel = fmod, qmodel = qmod)
NW.q3r <- residuals(NW.q3f, NW.stk, NW.idx2)
NW.q3s <- NW.stk + simulate(NW.q3f, 500)
NW.q3mc <- a4aSCA(NW.stk, NW.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
NW.q3mcmc <- as.mcmc(NW.q3mc)
NW.q3smc <- NW.stk + NW.q3mc
```

```
plot(NW.q3r)
```

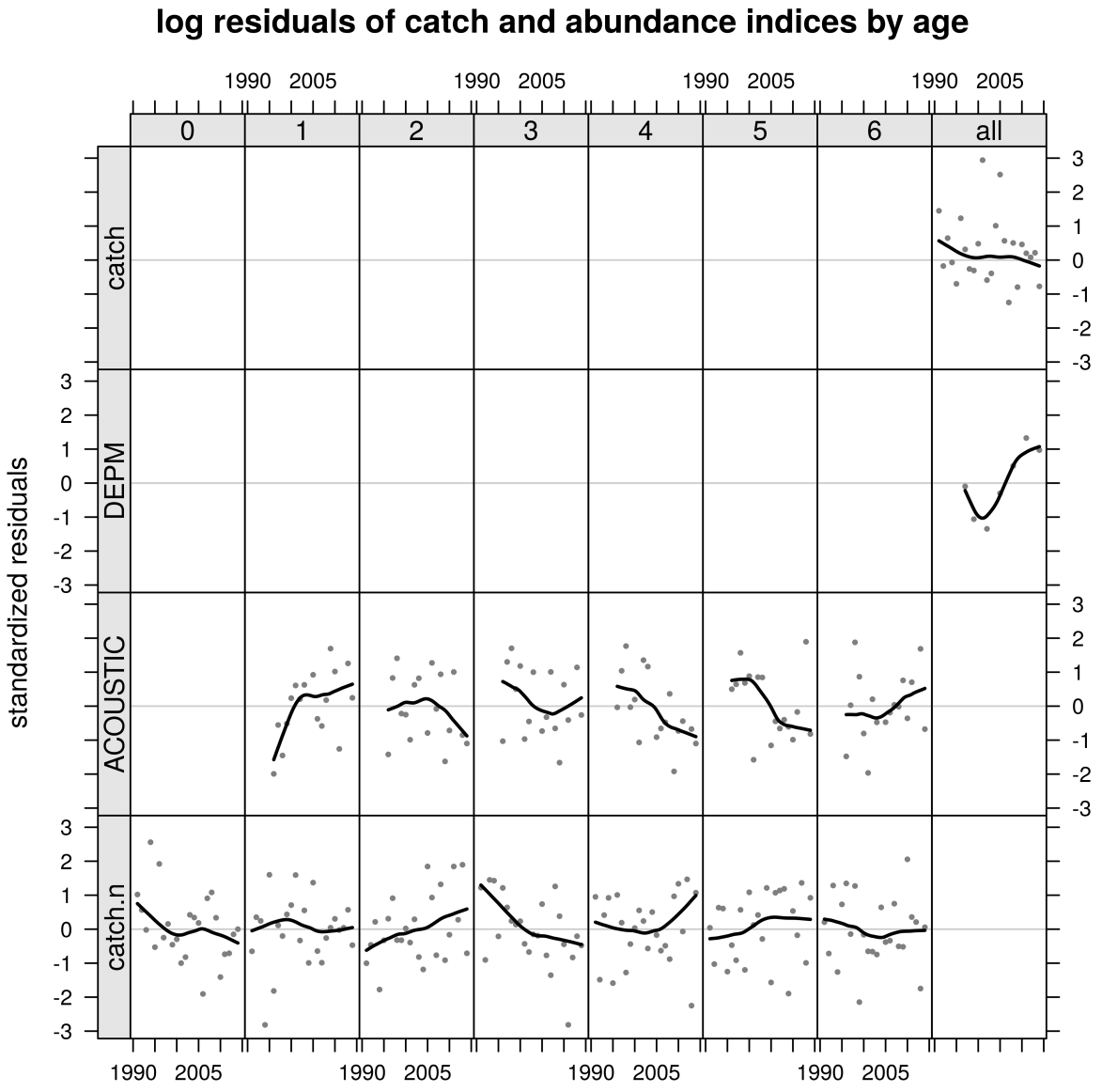

Figure 89: Residuals

```
plot(NW.q3f, NW.stk)
```

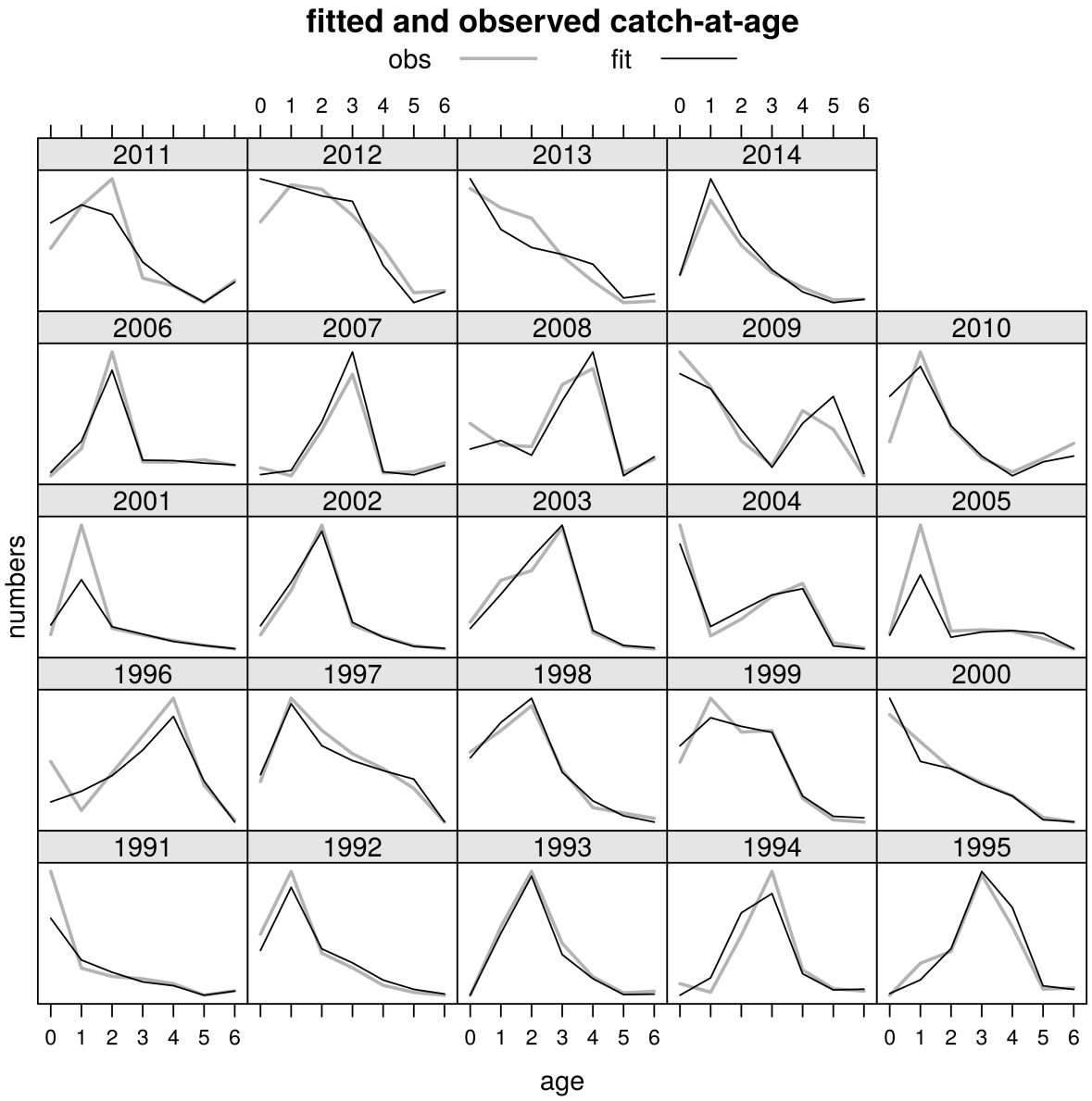

Figure 90: Catch-at-age predictions and observations

```
plot(NW.q3f, NW.idx2[1])
```

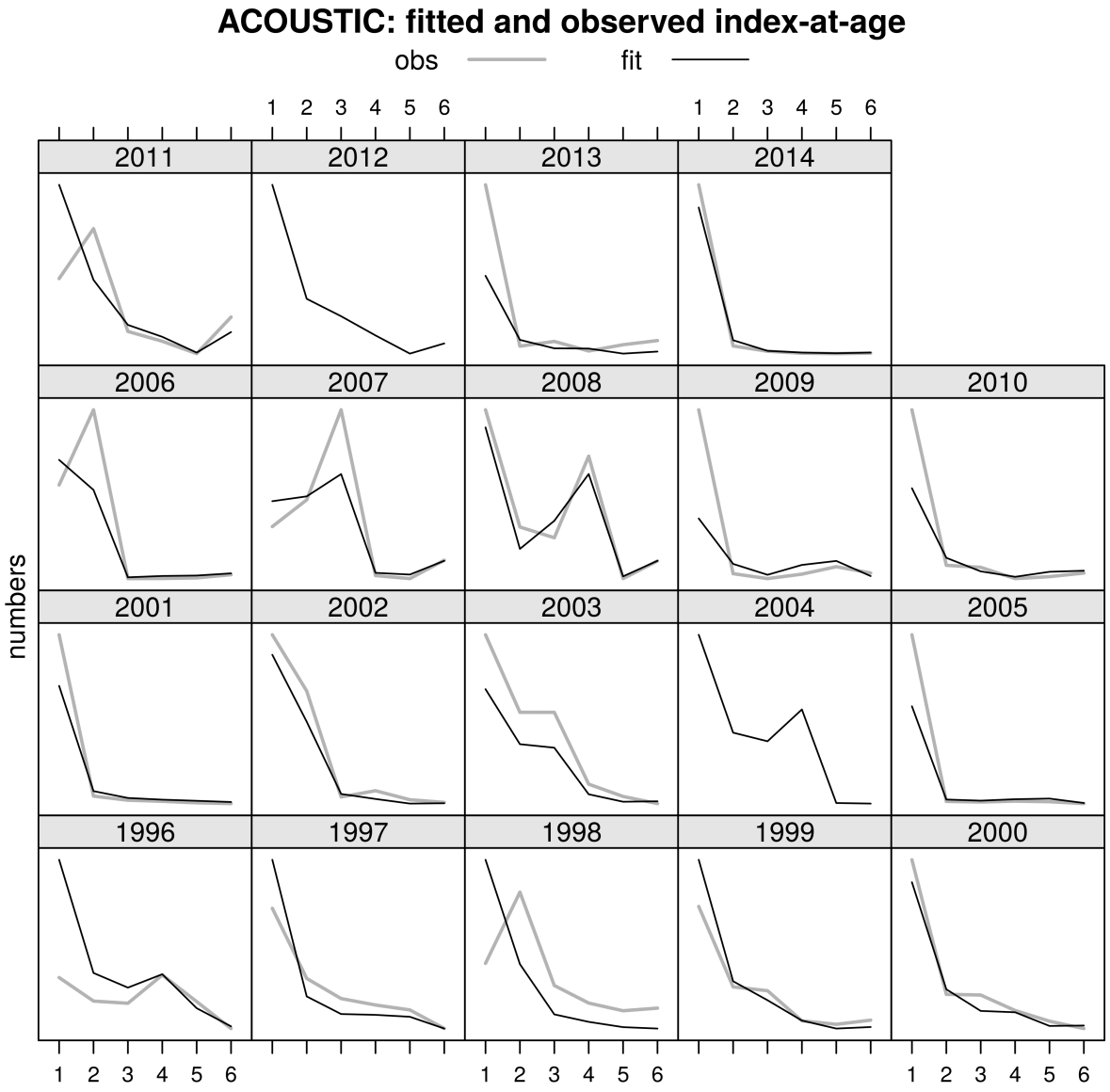

Figure 91: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(NW.q3f))
```

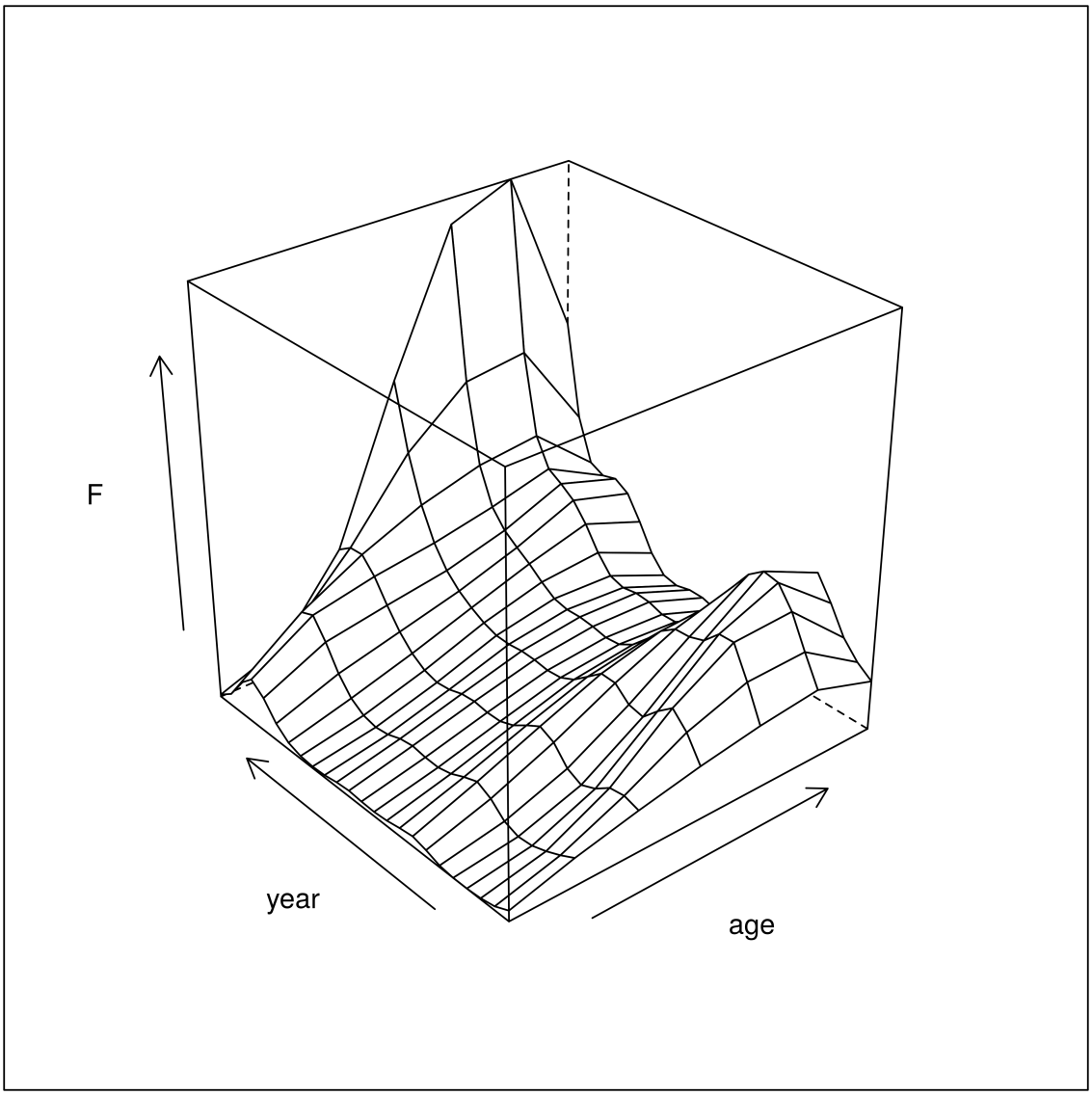

Figure 92: F-at-age estimate

```
plot(NW.q3mc)
```

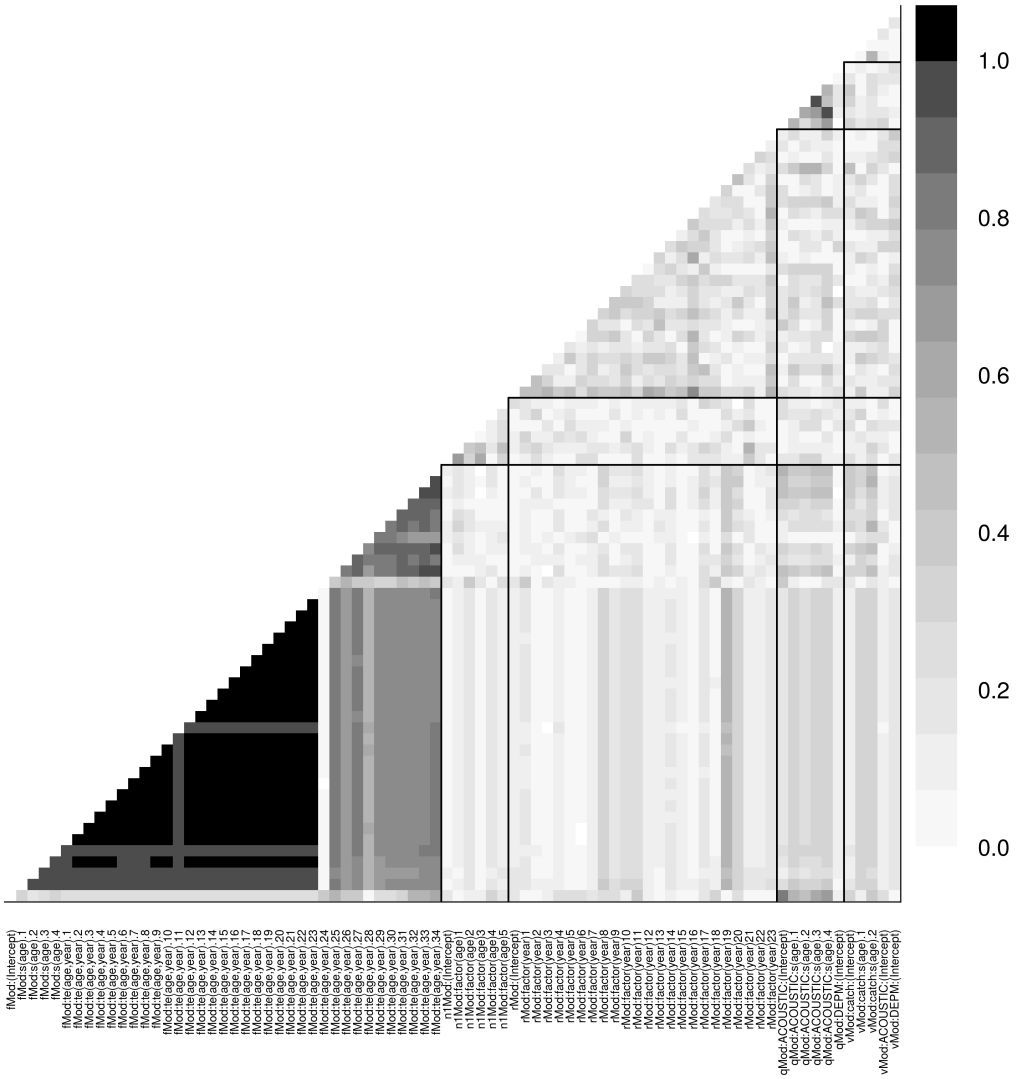

Figure 93: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(NW.q3smc)
```

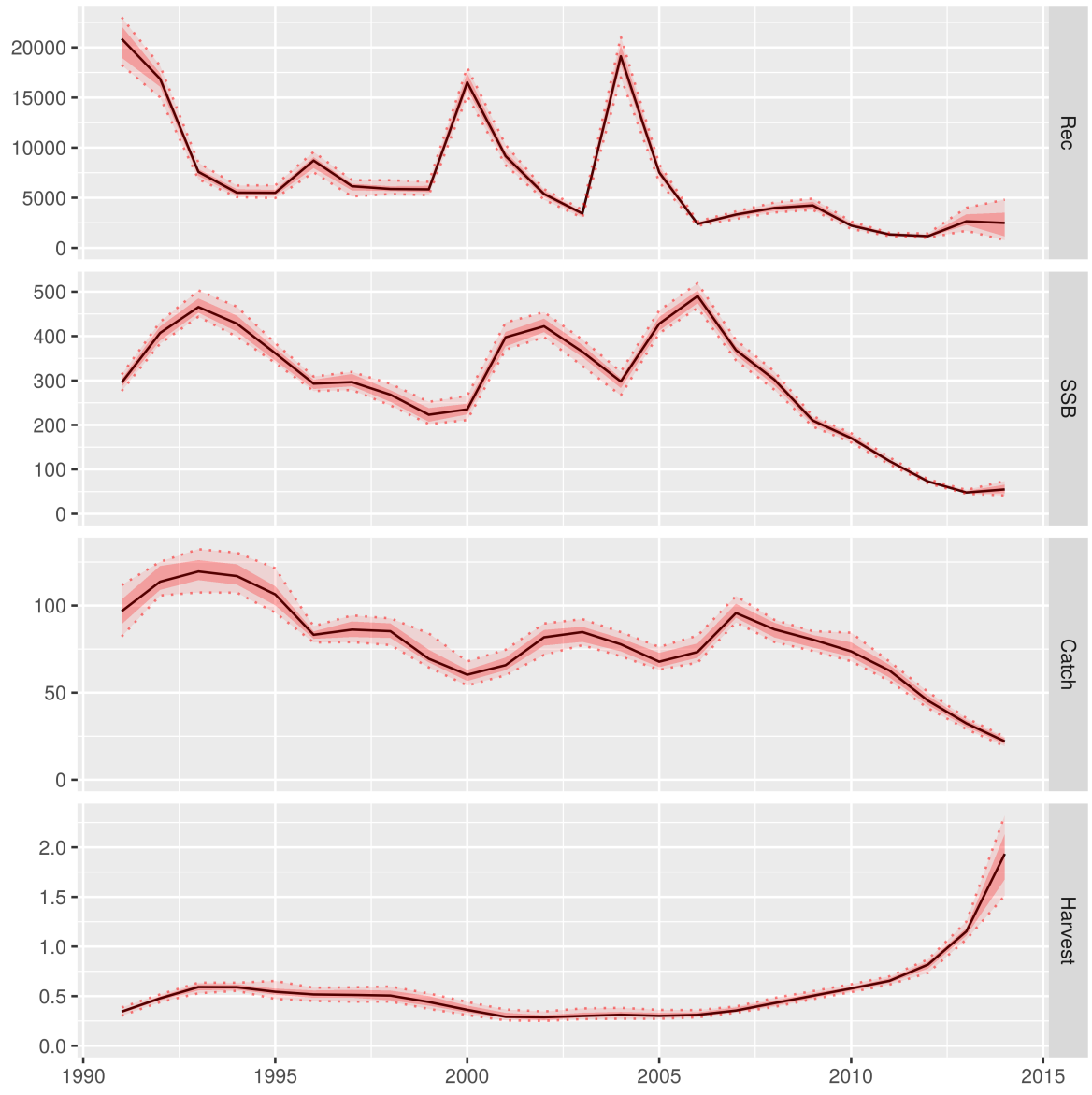

Figure 94: Summary plot

5.5.4 q option 4: constant, survey overweighting

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 12))
qmod <- list(~1, ~1)
NW.idx2 <- NW.idx
index.var(NW.idx2[[1]]) <- 0.5
NW.q4f <- a4aSCA(NW.stk, NW.idx2, fmodel = fmod, qmodel = qmod)
NW.q4r <- residuals(NW.q4f, NW.stk, NW.idx2)
NW.q4s <- NW.stk + simulate(NW.q4f, 500)
NW.q4mc <- a4aSCA(NW.stk, NW.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
NW.q4mcmc <- as.mcmc(NW.q4mc)
NW.q4smc <- NW.stk + NW.q4mc
```

```
plot(NW.q4r)
```

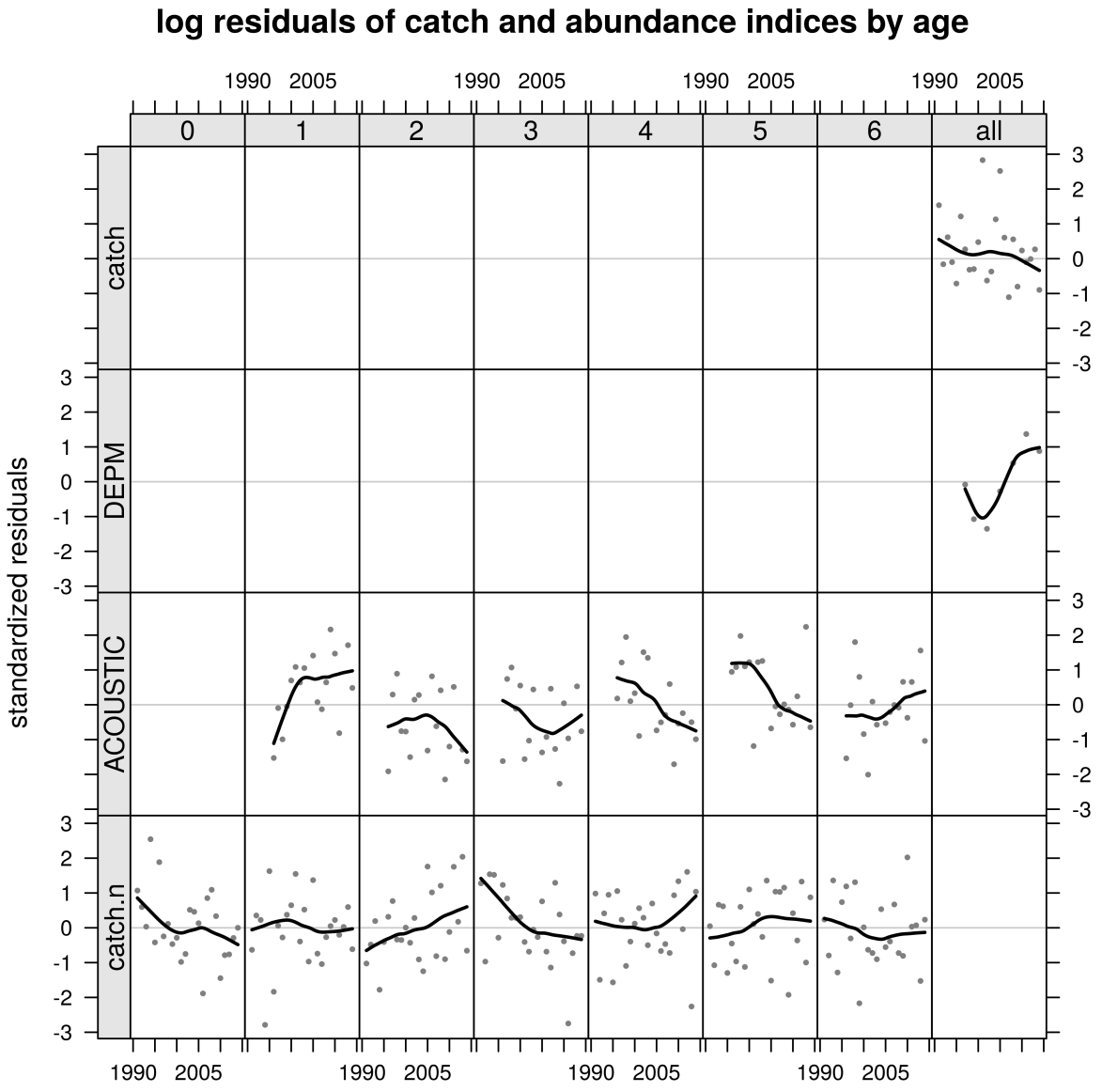

Figure 95: Residuals

```
plot(NW.q4f, NW.stk)
```

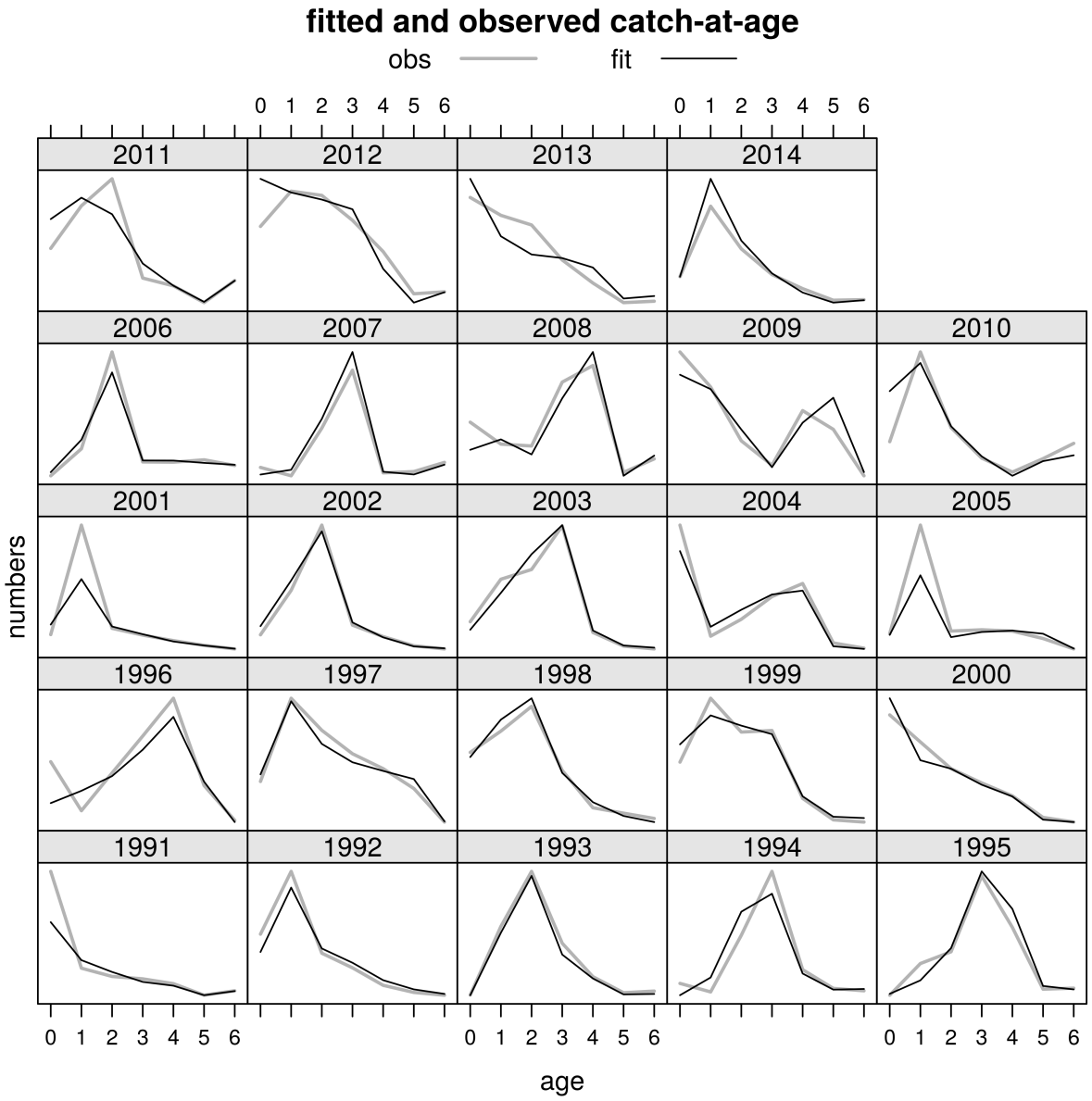

Figure 96: Catch-at-age predictions and observations

```
plot(NW.q4f, NW.idx2[1])
```

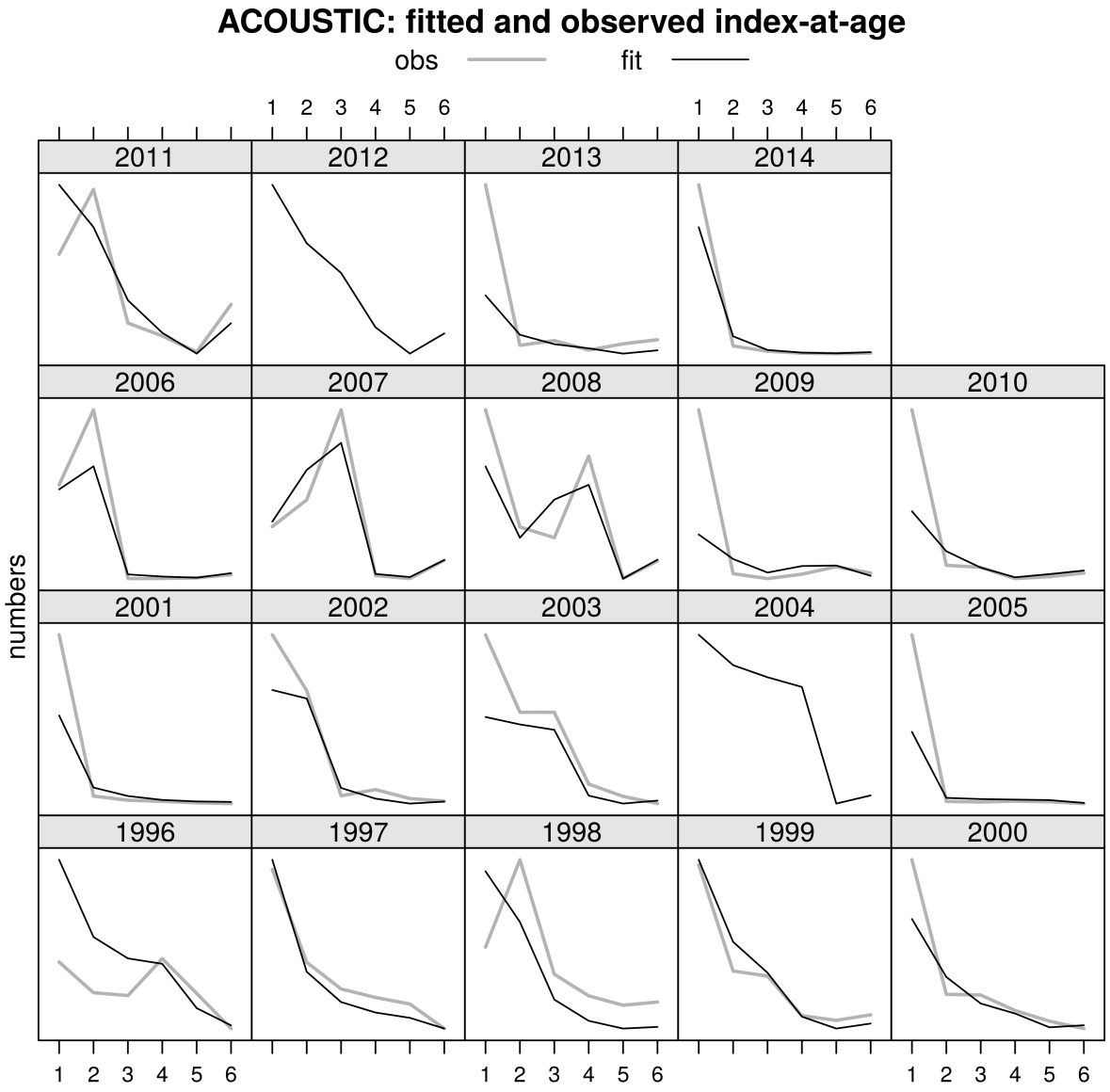

Figure 97: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(NW.q4f))
```

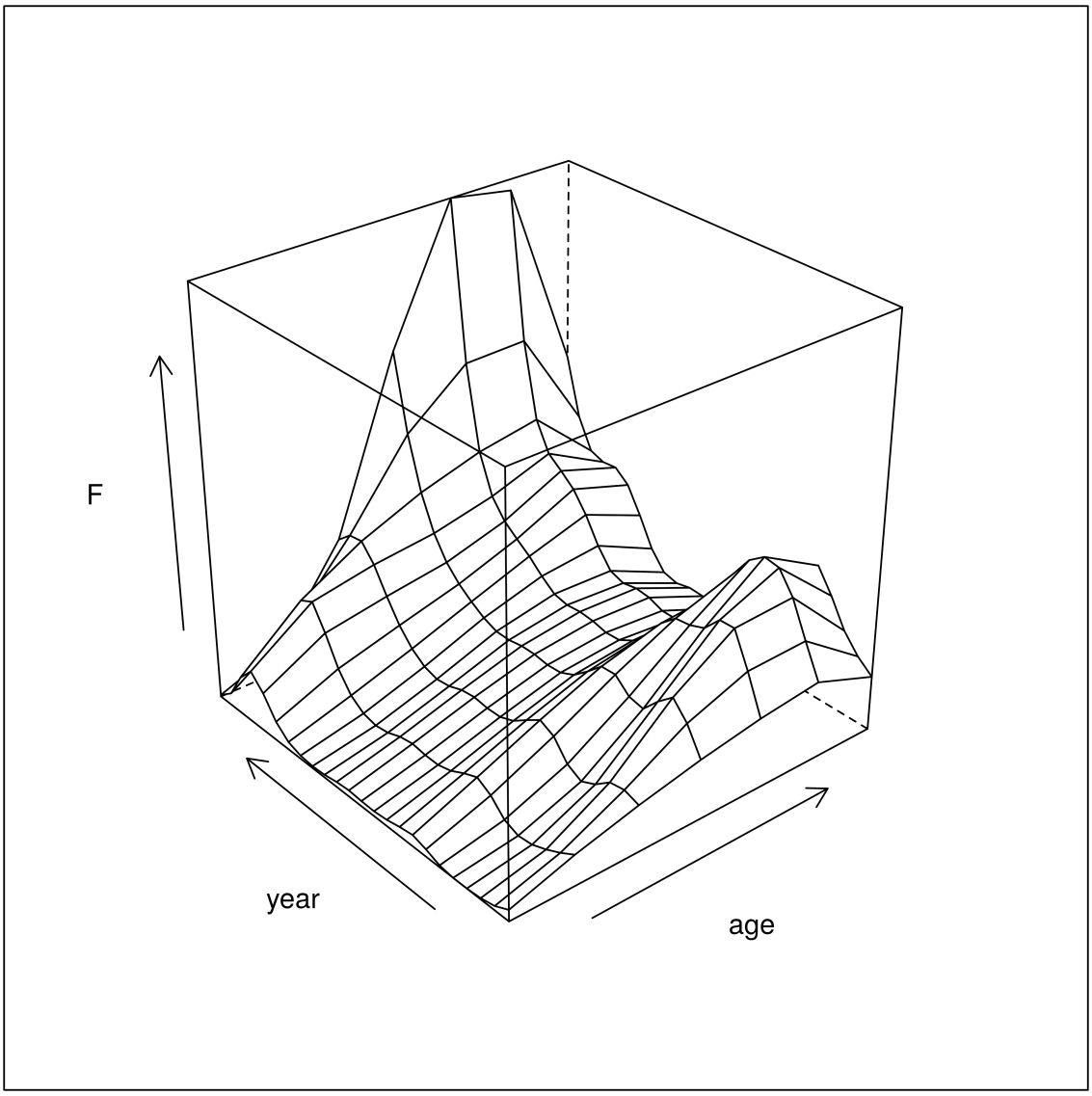

Figure 98: F-at-age estimate

```
plot(NW.q4mc)
```

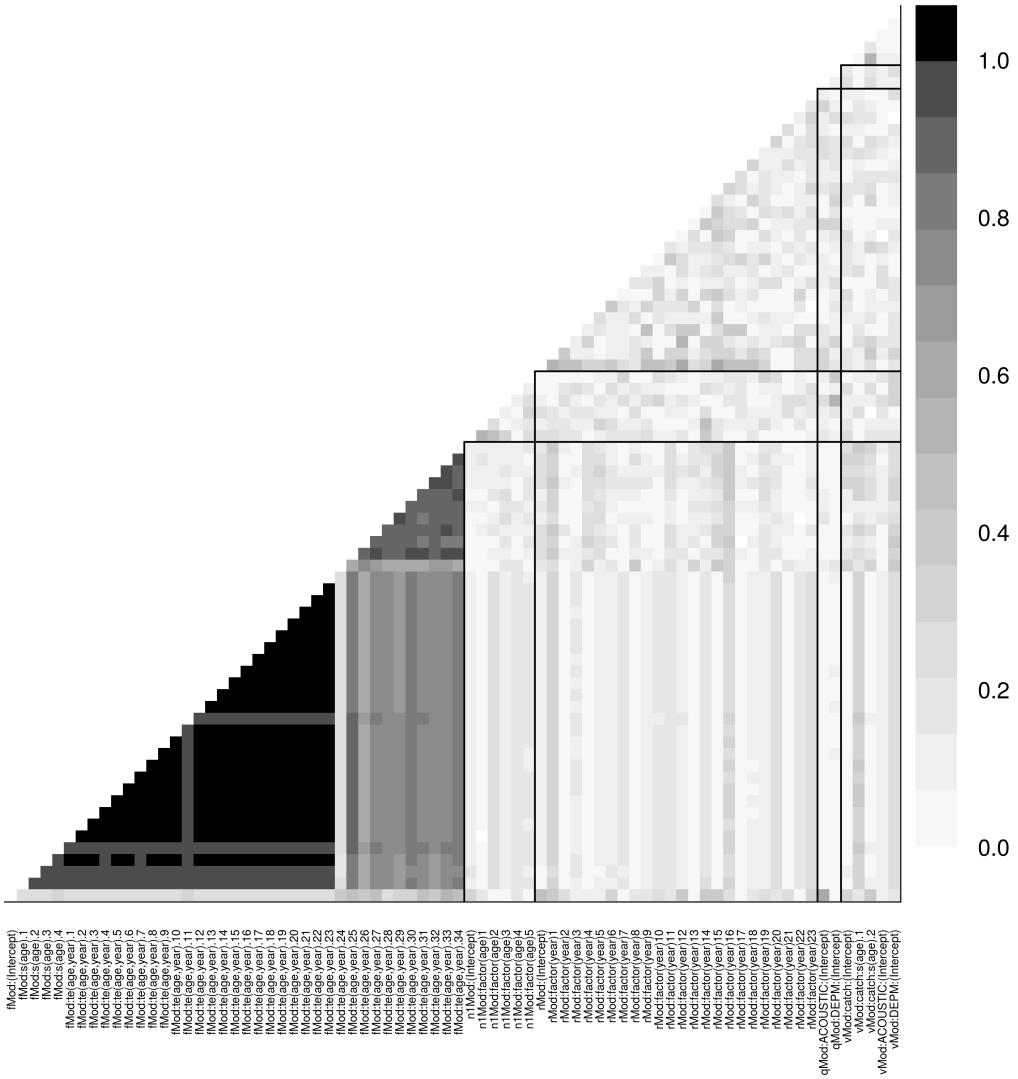

Figure 99: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(NW.q4smc)
```

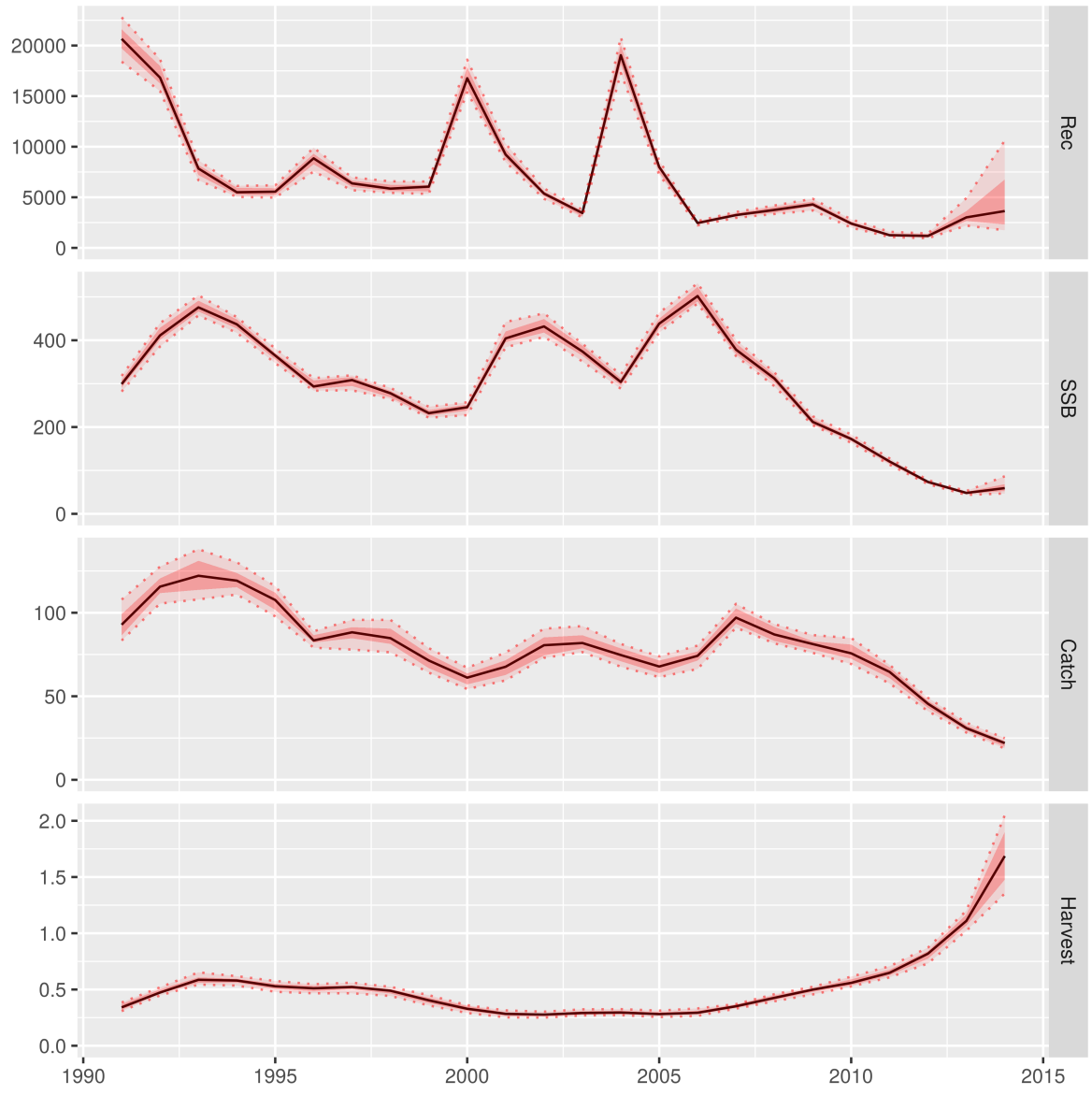

Figure 100: Summary plot

5.5.5 q option 5: constant, no overweighting of survey, no DEPM

```
fmod <- ~s(age, k = 5) + te(age, year, k = c(3, 12))
qmod <- list(~1)
NW.q5f <- a4aSCA(NW.stk, NW.idx[1], fmodel = fmod, qmodel = qmod)
NW.q5r <- residuals(NW.q5f, NW.stk, NW.idx[1])
NW.q5s <- NW.stk + simulate(NW.q5f, 500)
NW.q5mc <- a4aSCA(NW.stk, NW.idx[1], fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
NW.q5mcmc <- as.mcmc(NW.q5mc)
NW.q5smc <- NW.stk + NW.q5mc
```

```
plot(NW.q5r)
```

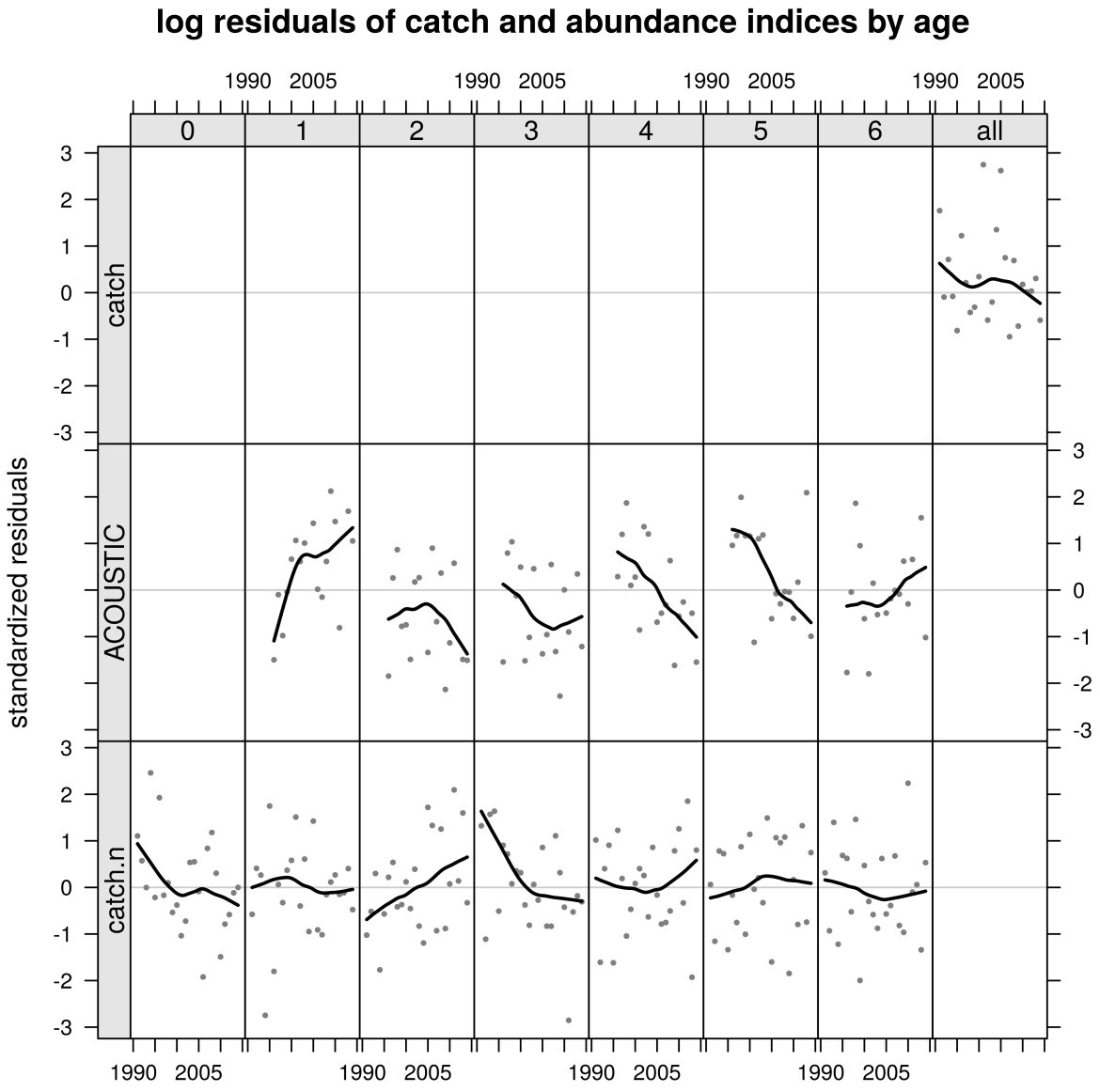

Figure 101: Residuals

```
plot(NW.q5f, NW.stk)
```

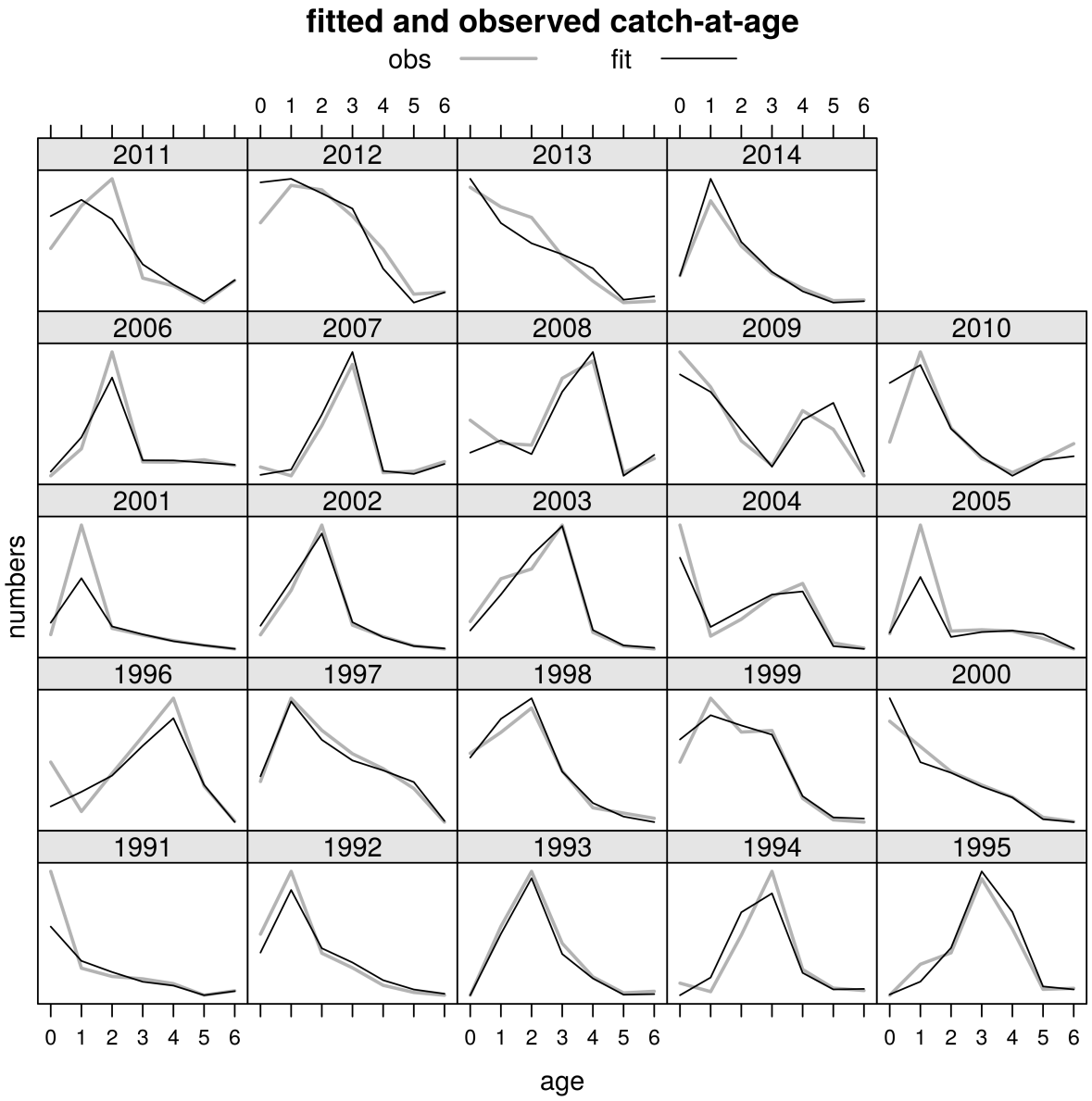

Figure 102: Catch-at-age predictions and observations

```
plot(NW.q5f, NW.idx[1])
```

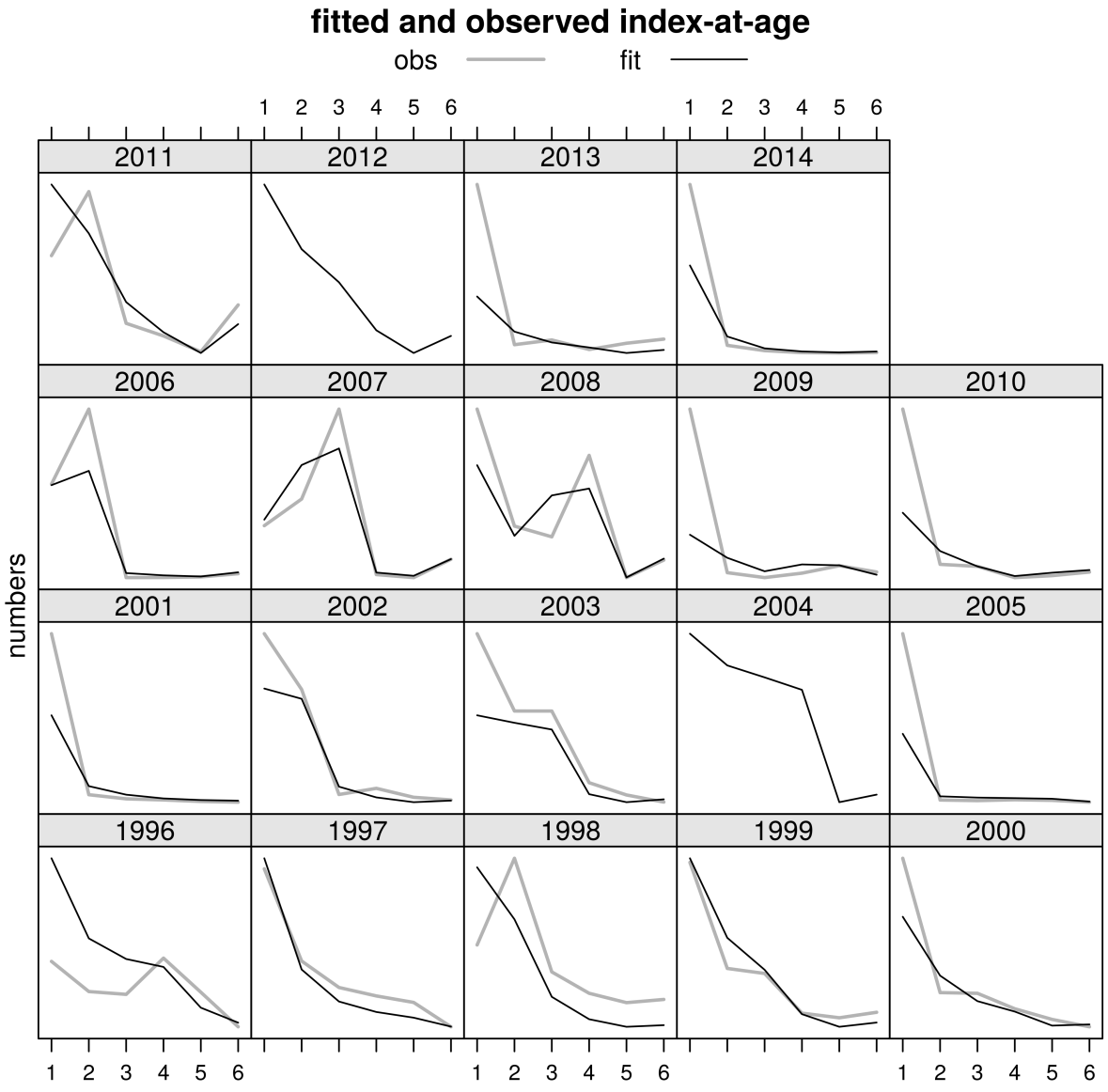

Figure 103: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(NW.q5f))
```

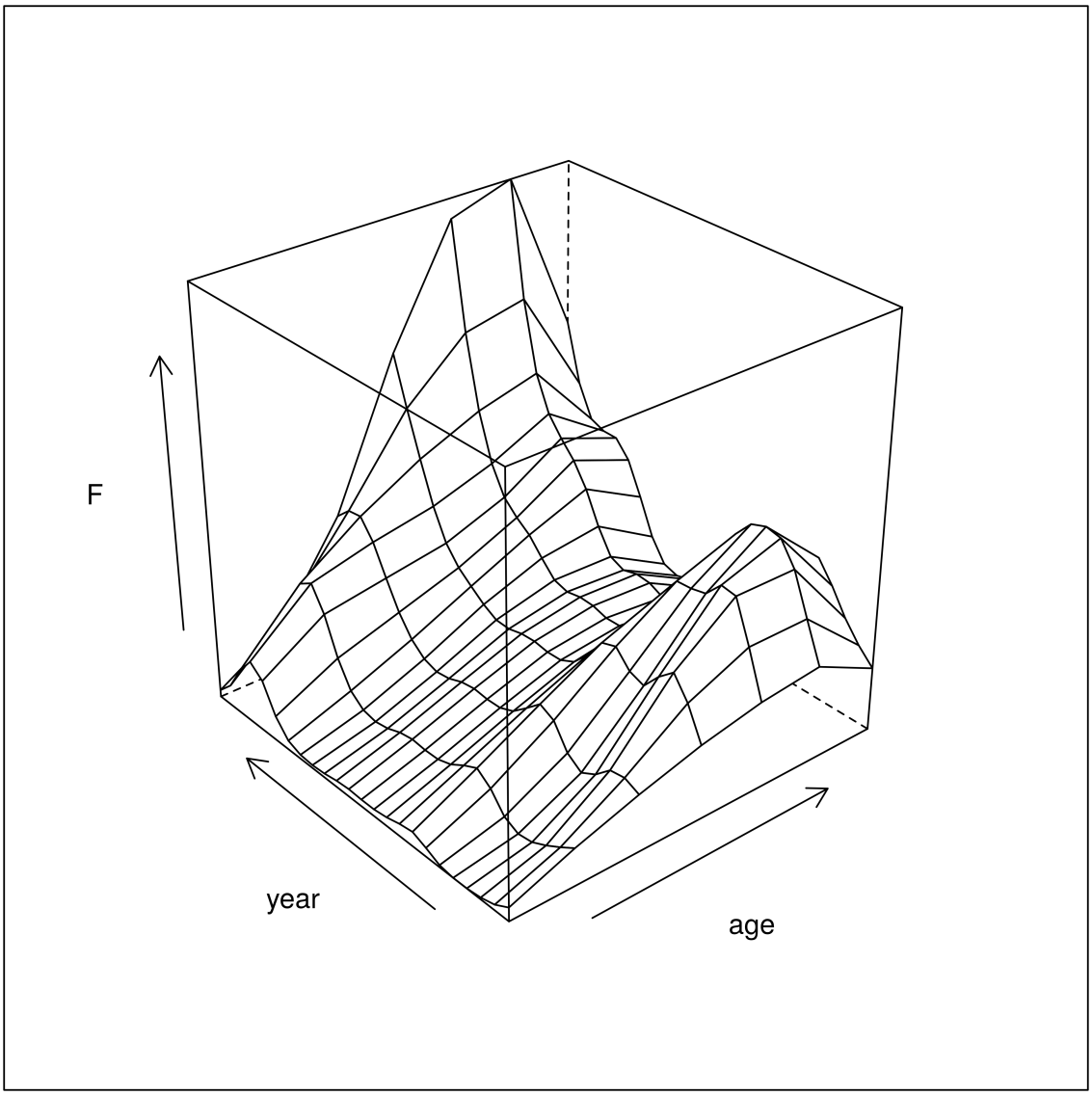

Figure 104: F-at-age estimate

```
plot(NW.q5mc)
```

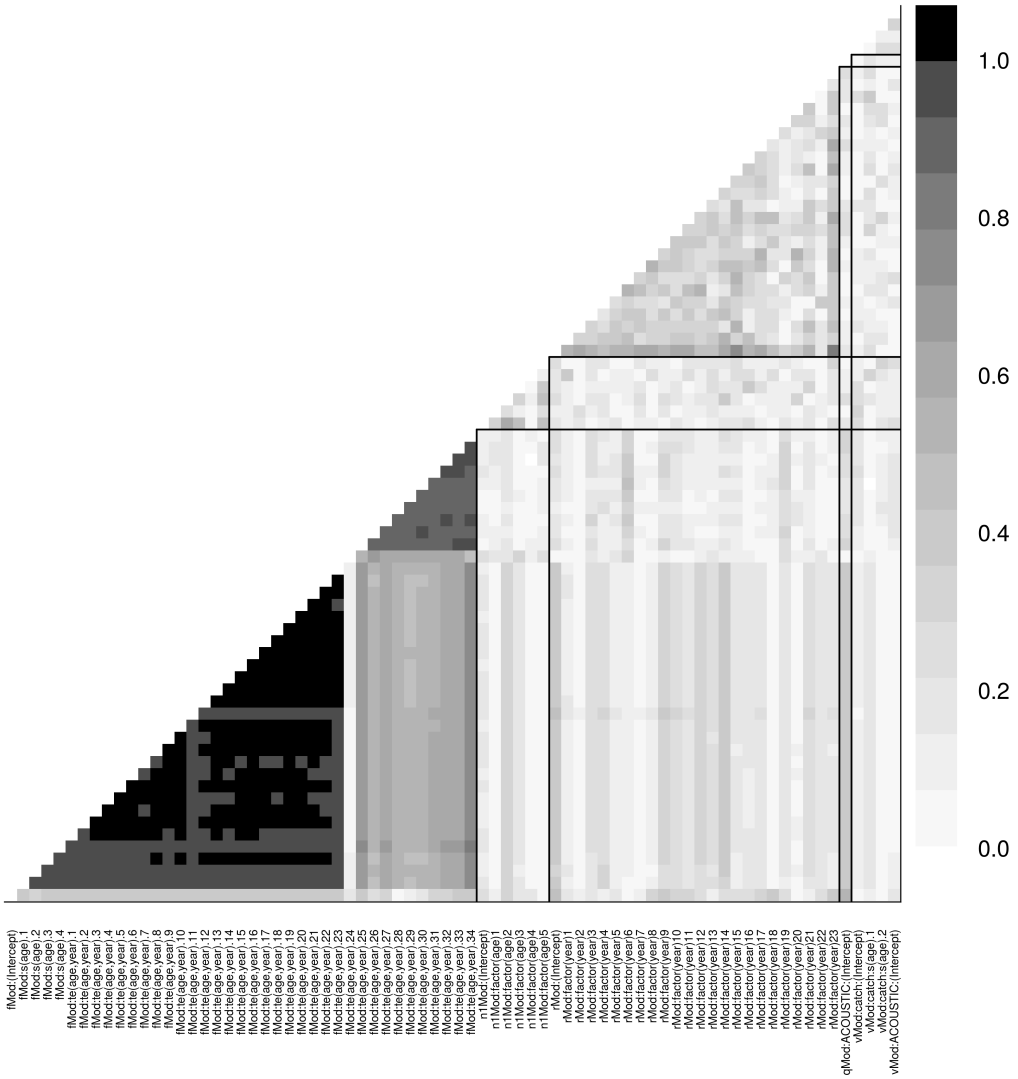

Figure 105: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(NW.q5smc)
```

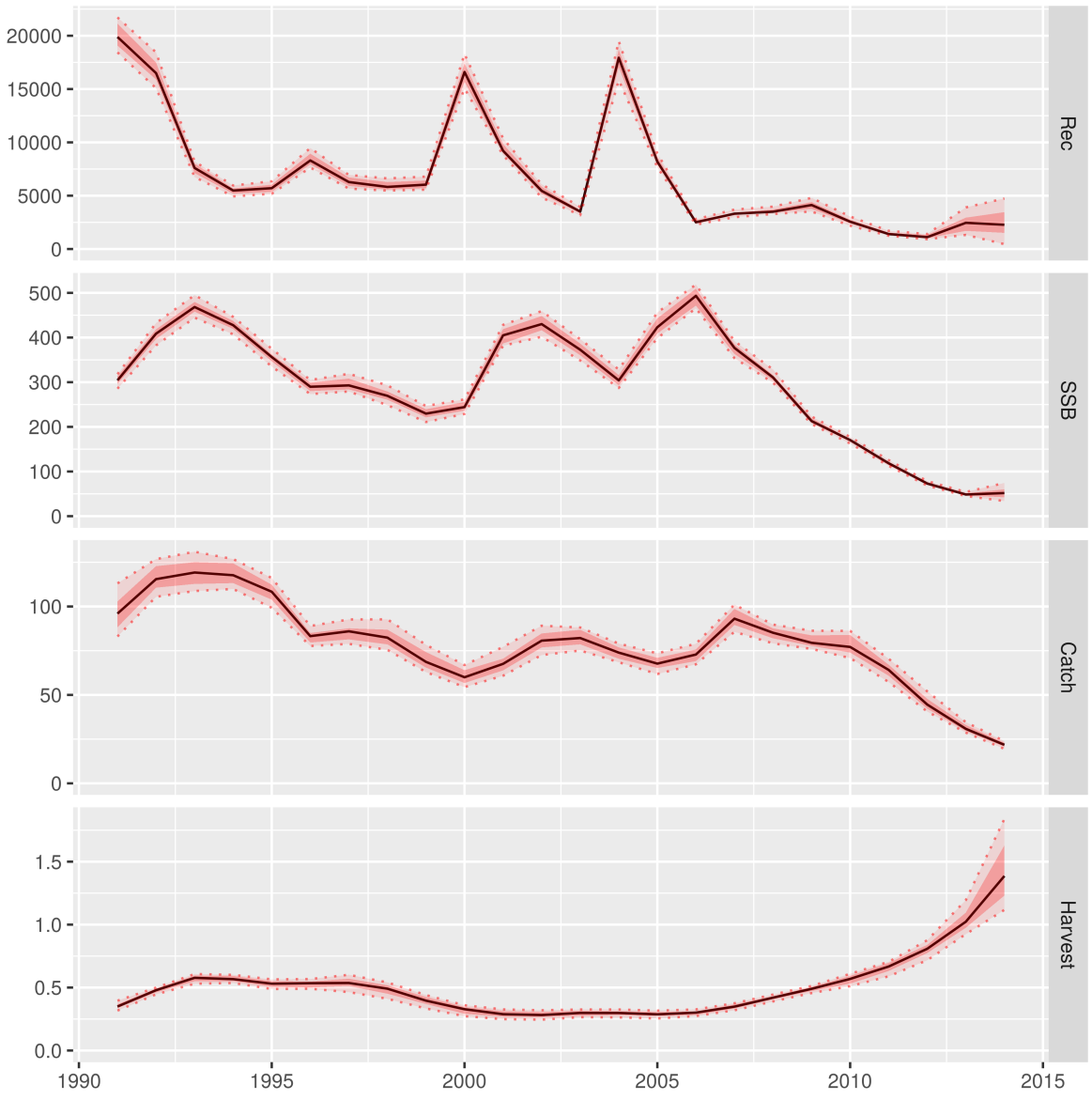

Figure 106: Summary plot

5.5.6 Comparison across assessments

```
plot(FLStocks(q1 = NW.q1smc, q2 = NW.q2smc, q3 = NW.q3smc, q4 = NW.q4smc,
    q5 = NW.q5smc))
```

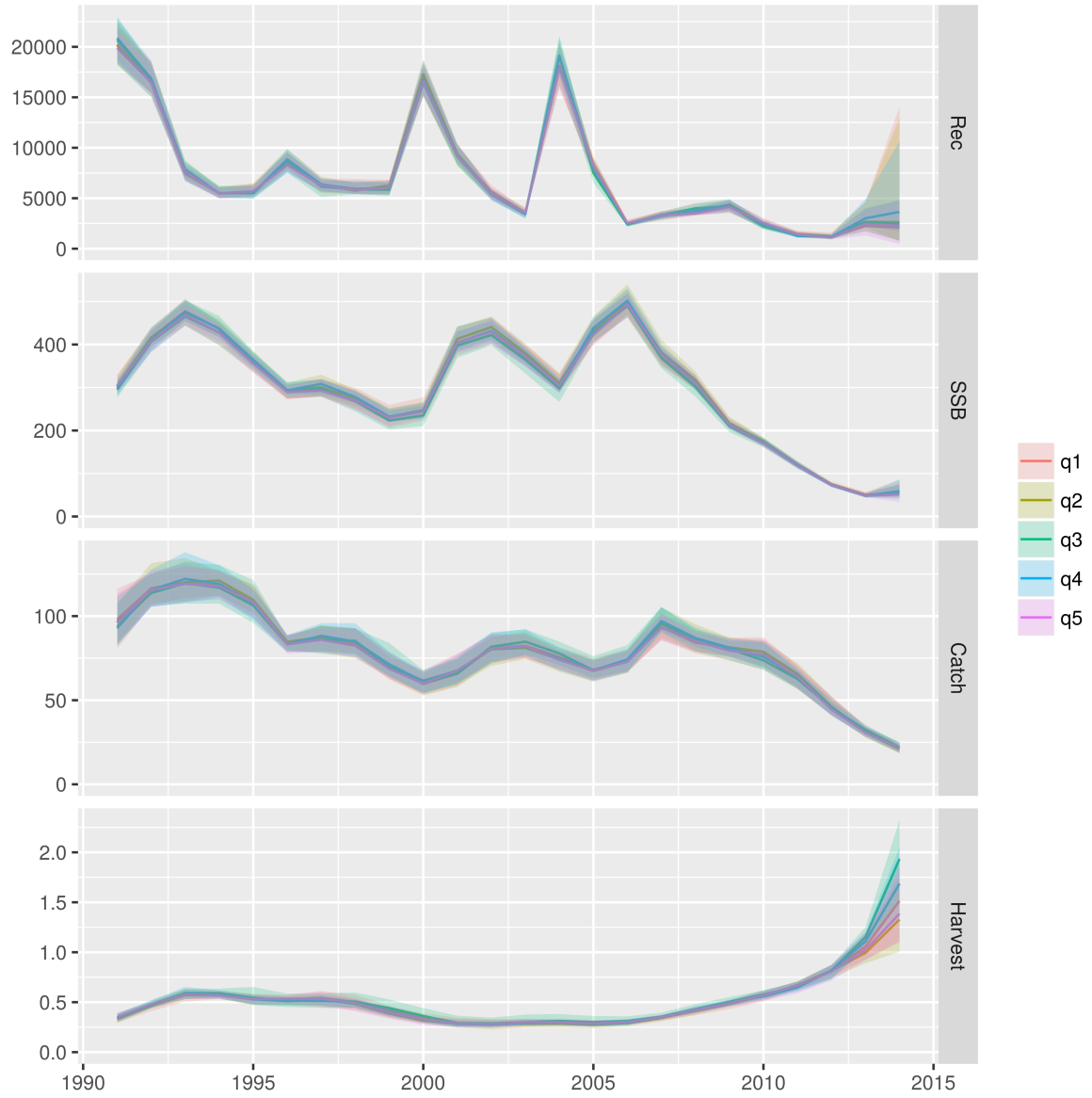

Figure 107: All assessments summary

5.6 The Shouthern sub-unit

```
load("../analysis/S/S.RData")
```

5.6.1 q option 1: smoother, no overweighting of survey

```
fmod <- ~s(age, k = 4) + te(age, year, k = c(3, 15))
qmod <- list(~s(age, k = 5), ~1)
S.q1f <- a4aSCA(S.stk, S.idx, fmodel = fmod, qmodel = qmod)
S.q1r <- residuals(S.q1f, S.stk, S.idx)
S.q1s <- S.stk + simulate(S.q1f, 500)
S.q1mc <- a4aSCA(S.stk, S.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
S.q1mcmc <- as.mcmc(S.q1mc)
S.q1smc <- S.stk + S.q1mc
```

```
plot(S.q1r)
```

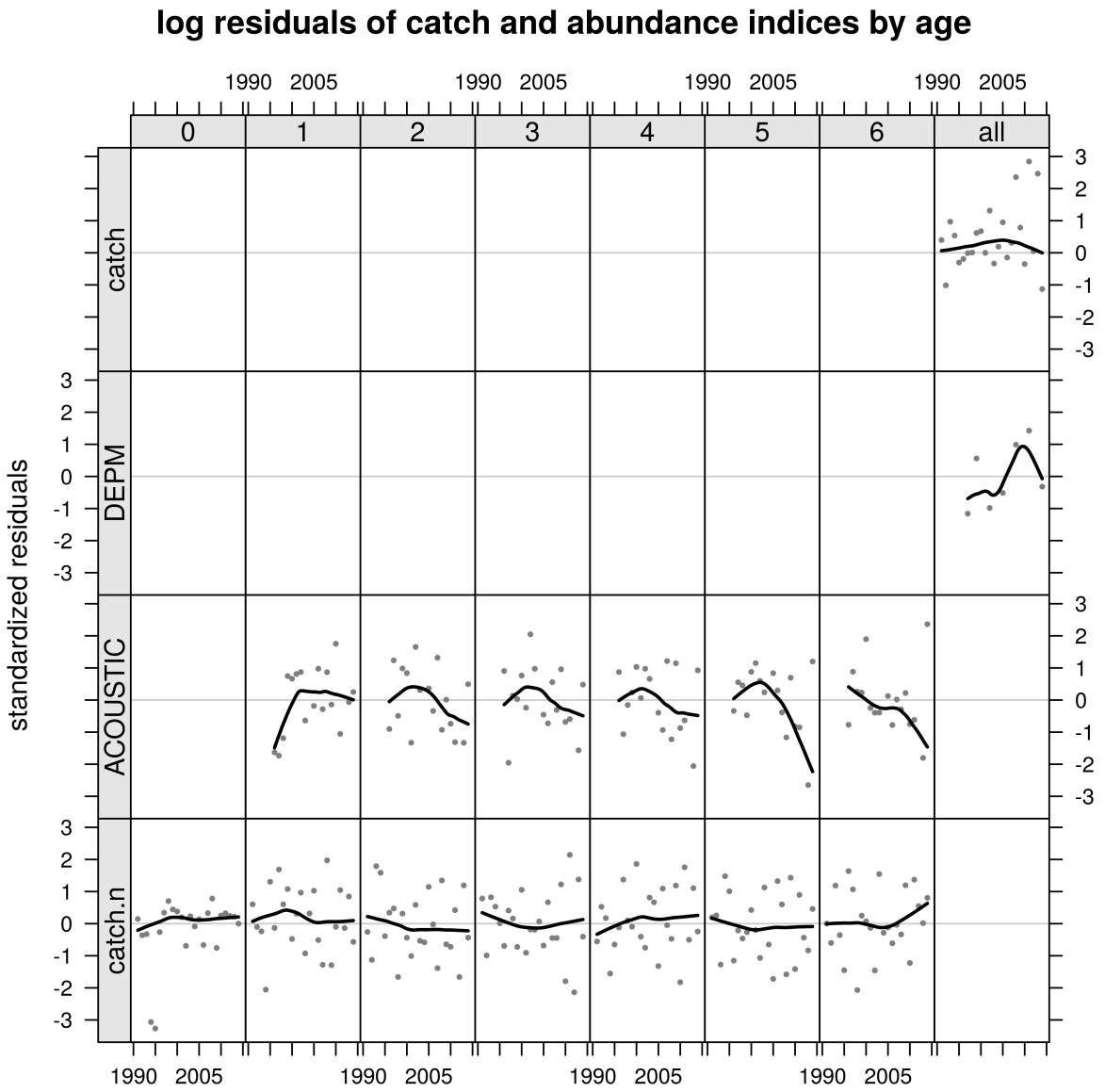

Figure 108: Residuals

```
plot(S.q1f, S.stk)
```

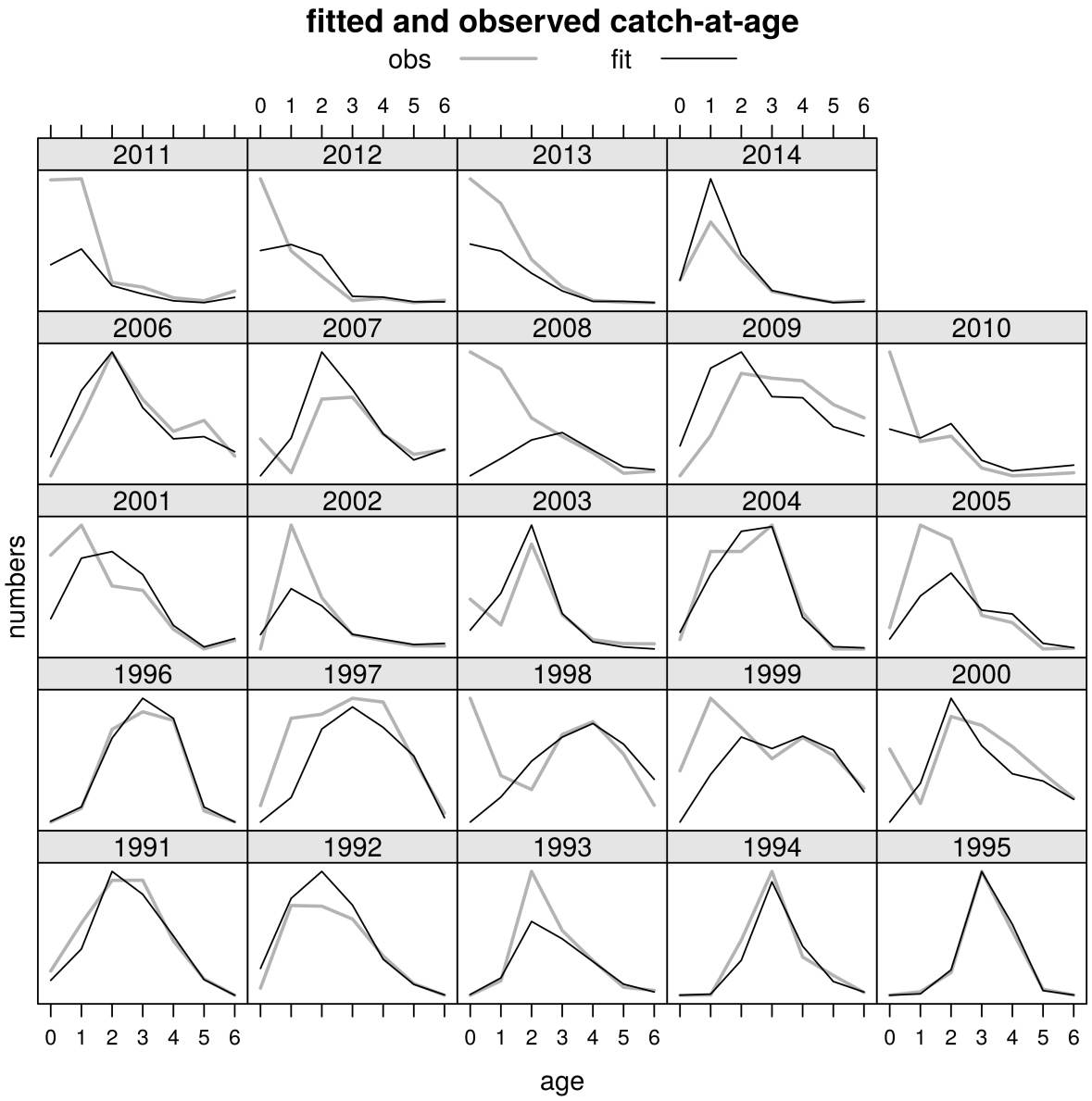

Figure 109: Catch-at-age predictions and observations

```
plot(S.q1f, S.idx[1])
```

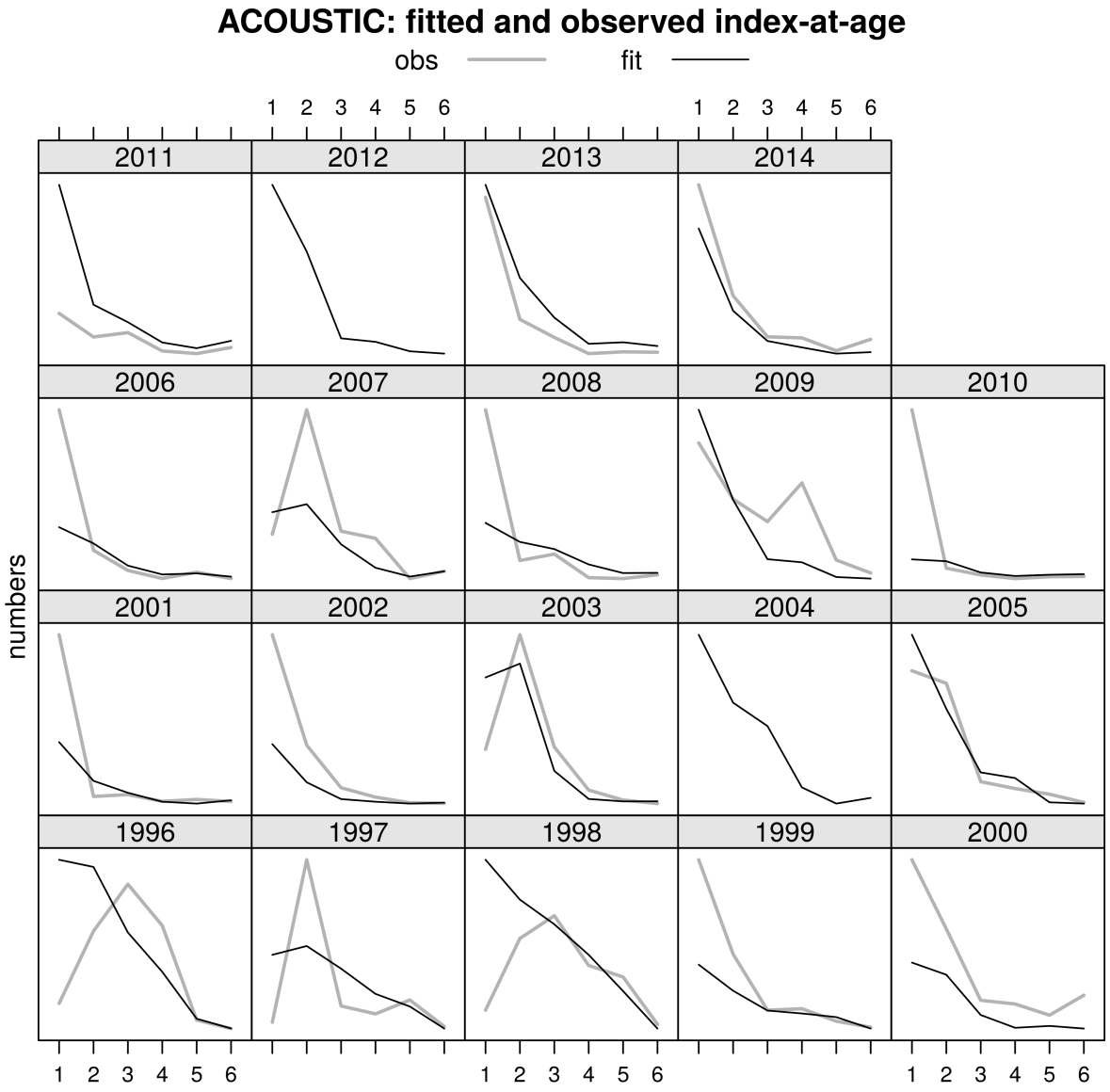

Figure 110: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(S.q1f))
```

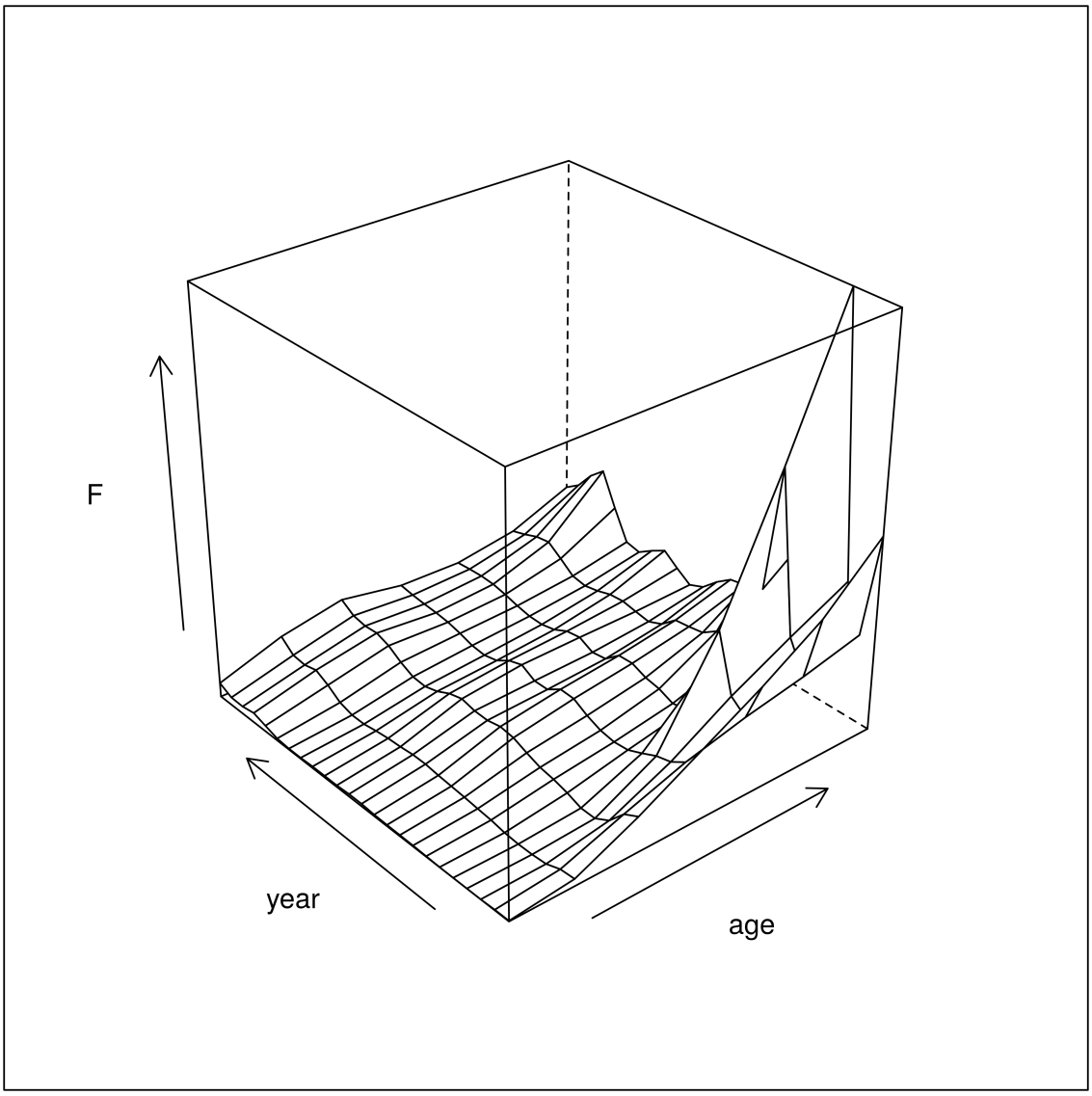

Figure 111: F-at-age estimate

```
plot(S.q1mc)
```

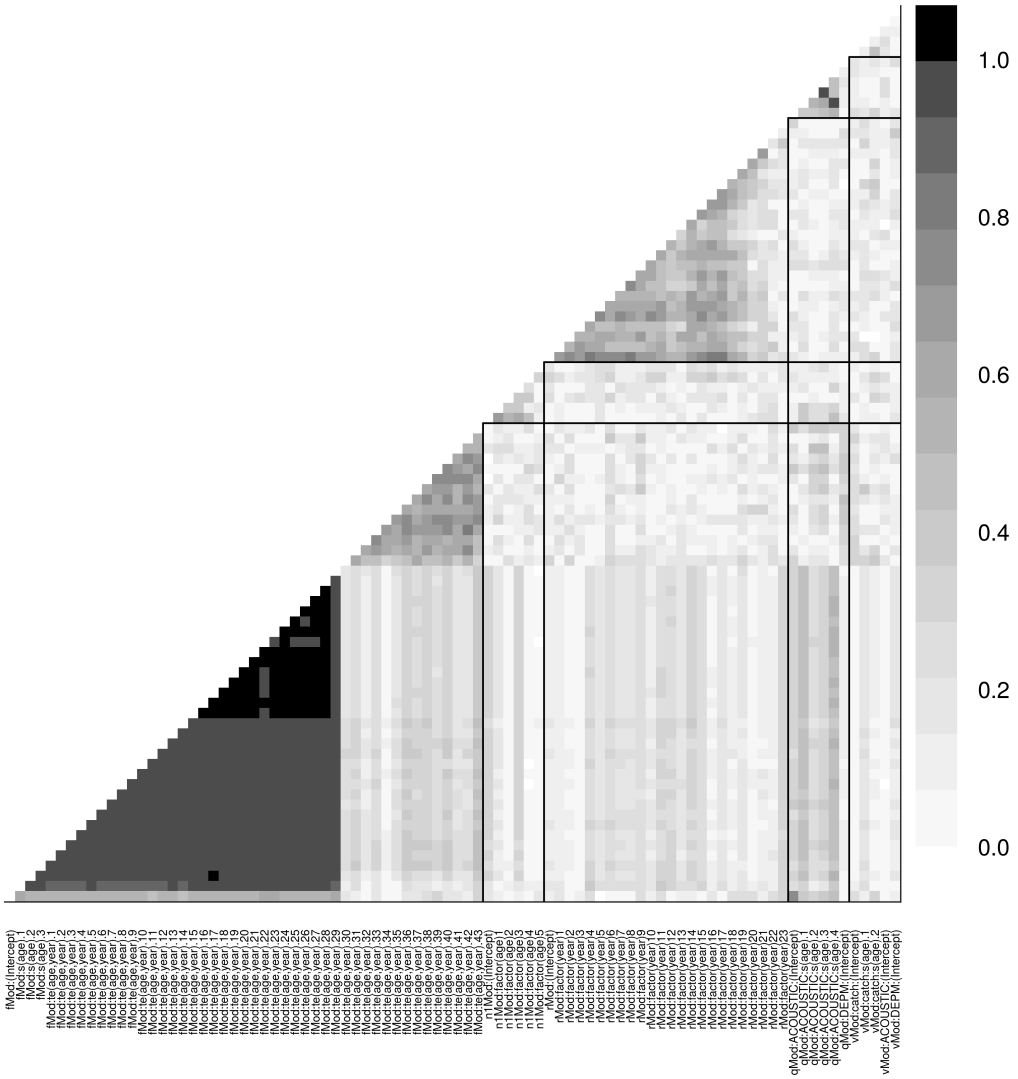

Figure 112: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(S.q1smc)
```

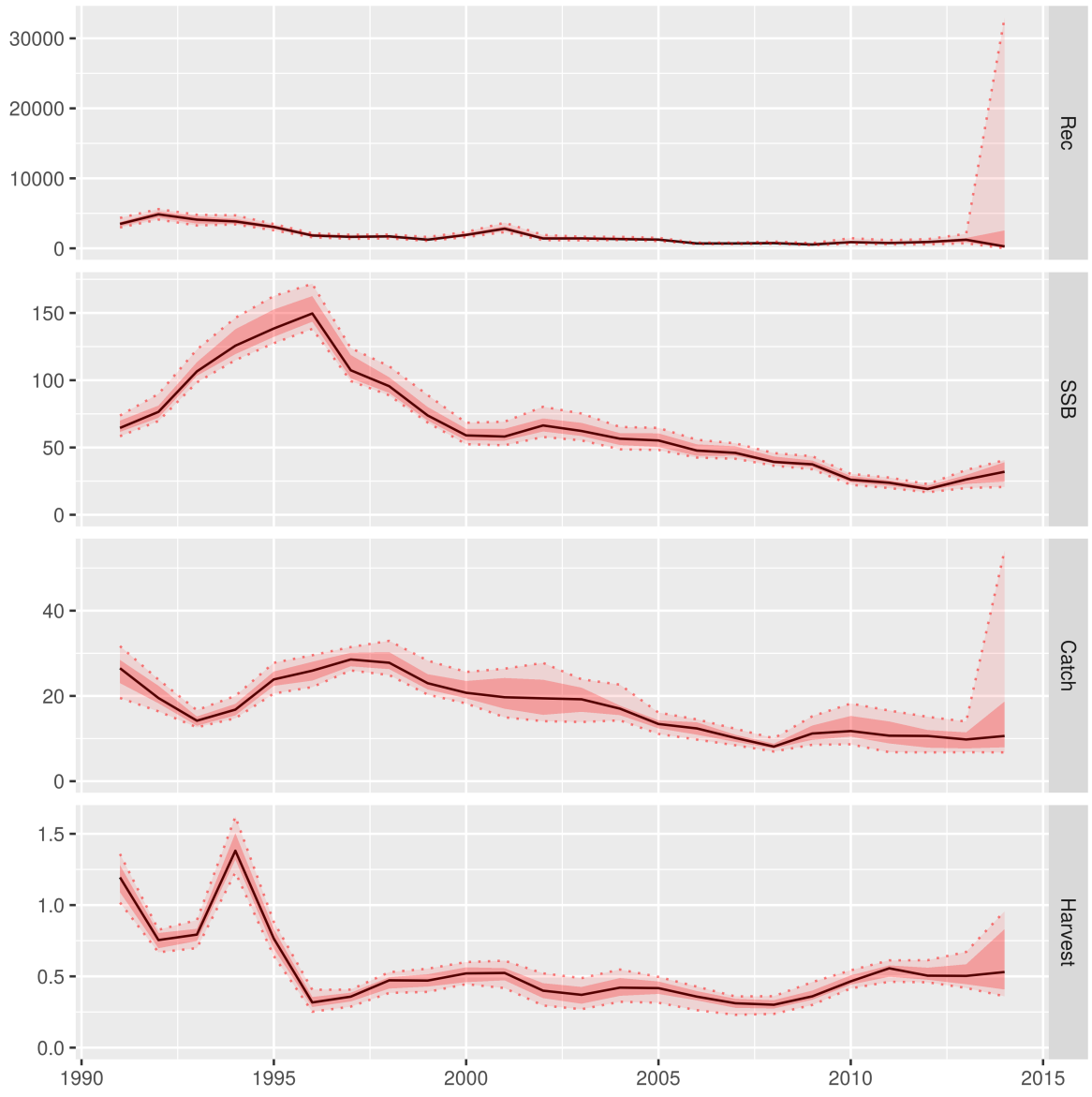

Figure 113: Summary plot

5.6.2 q option 2: constant, no overweighting of survey

```
fmod <- ~s(age, k = 4) + te(age, year, k = c(3, 15))
qmod <- list(~1, ~1)
S.q2f <- a4aSCA(S.stk, S.idx, fmodel = fmod, qmodel = qmod)
S.q2r <- residuals(S.q2f, S.stk, S.idx)
S.q2s <- S.stk + simulate(S.q2f, 500)
S.q2mc <- a4aSCA(S.stk, S.idx, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
S.q2mcmc <- as.mcmc(S.q2mc)
S.q2smc <- S.stk + S.q2mc
```

```
plot(S.q2r)
```

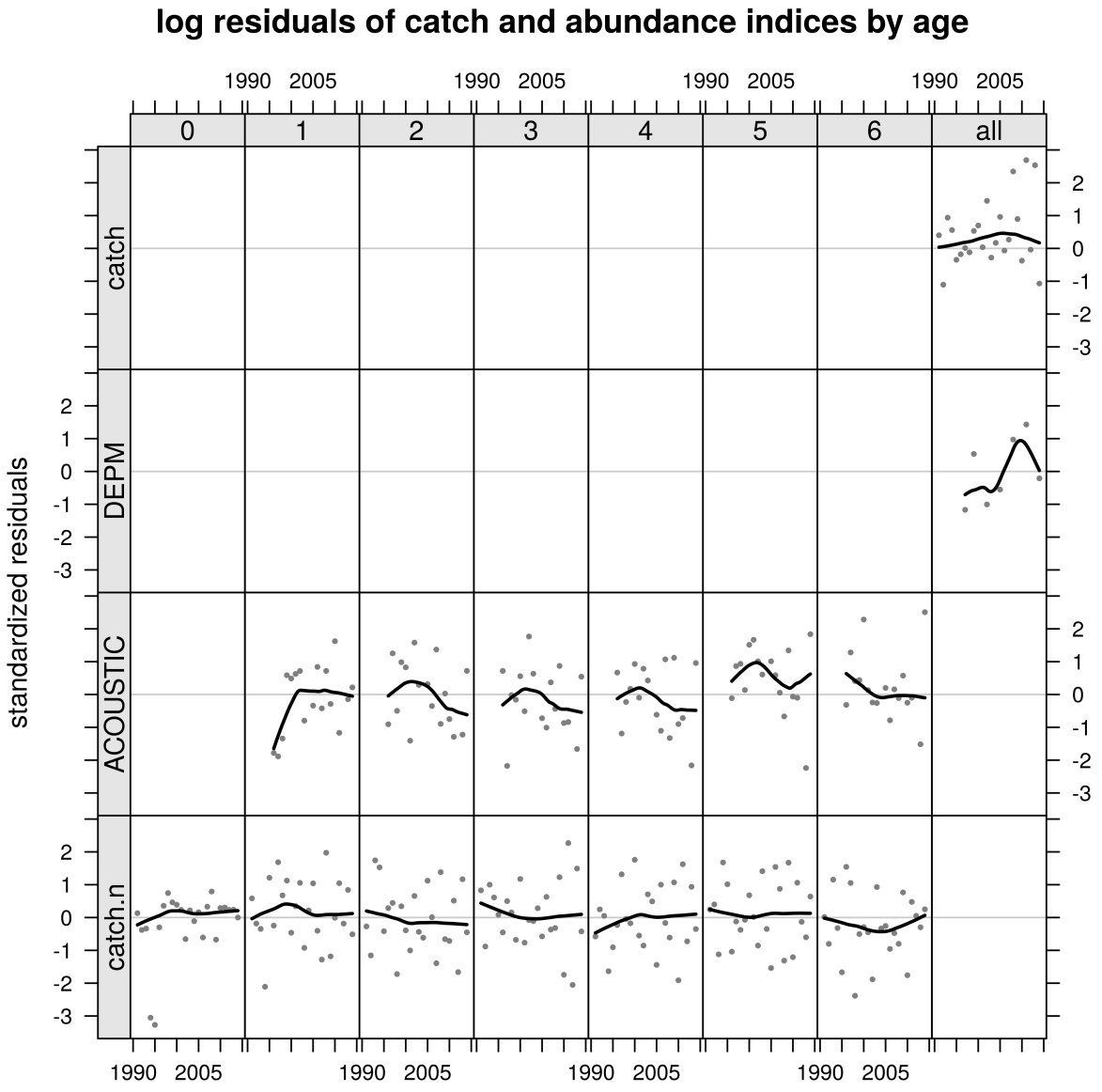

Figure 114: Residuals

```
plot(S.q2f, S.stk)
```

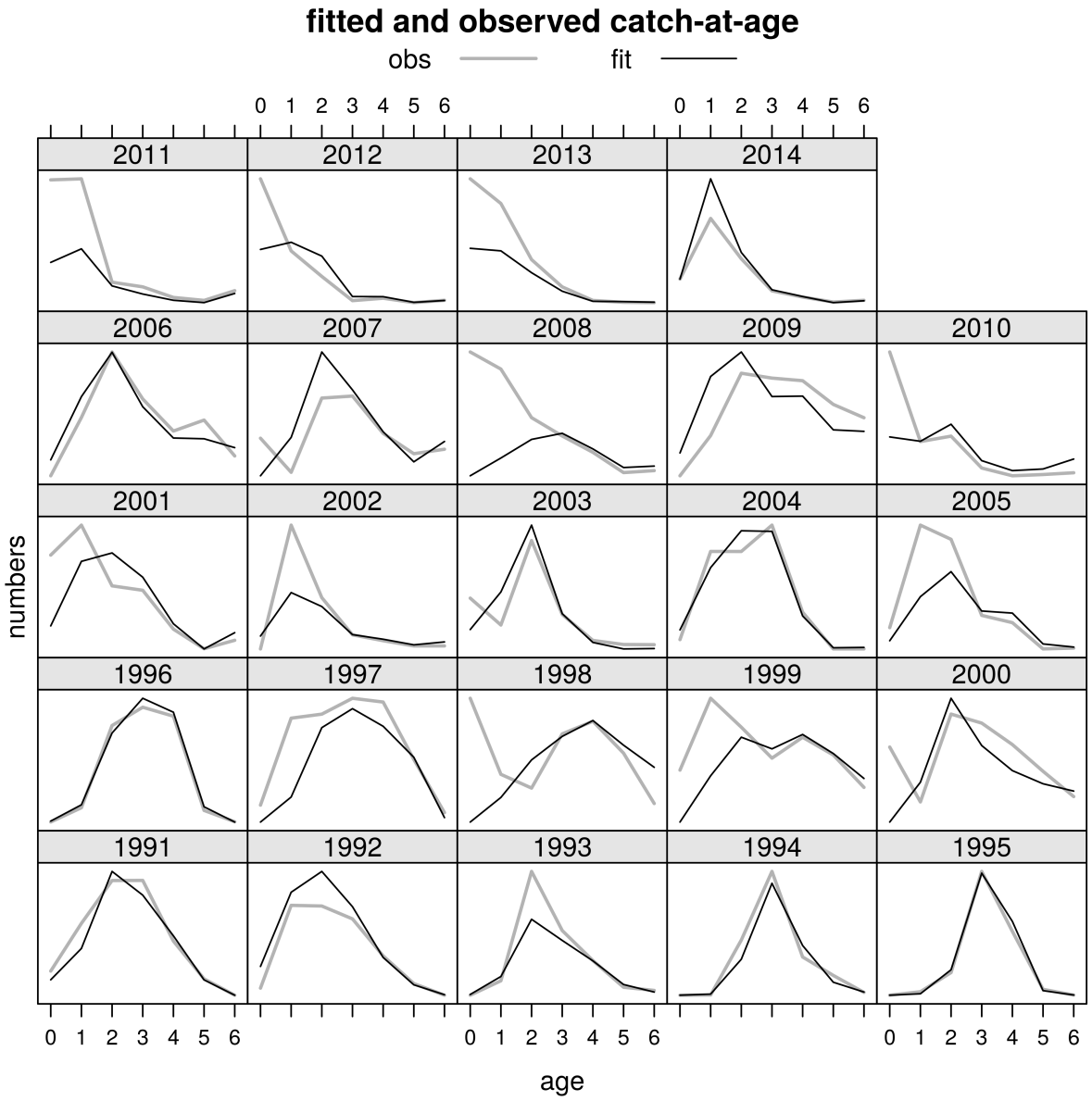

Figure 115: Catch-at-age predictions and observations

```
plot(S.q2f, S.idx[1])
```

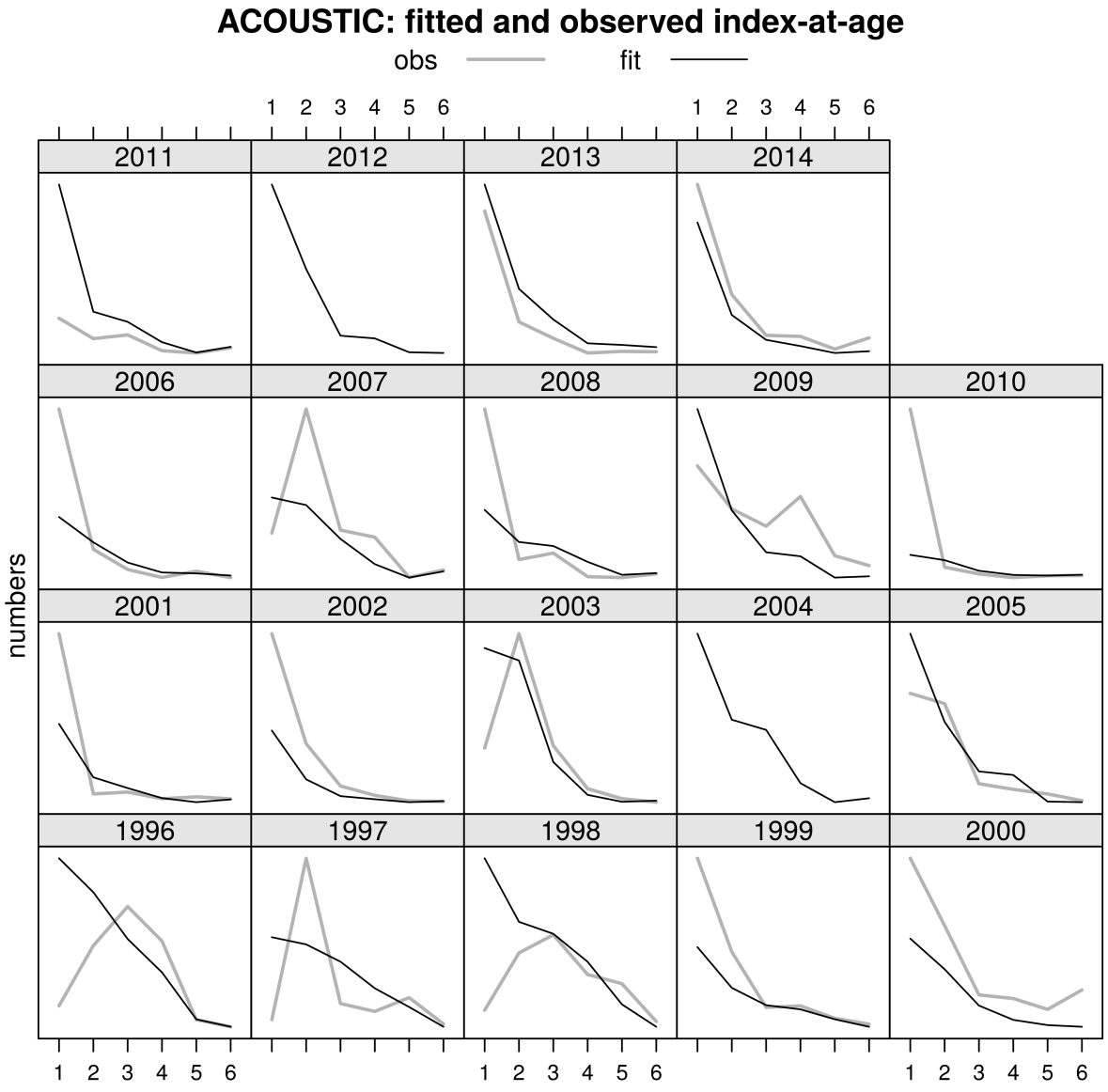

Figure 116: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(S.q2f))
```

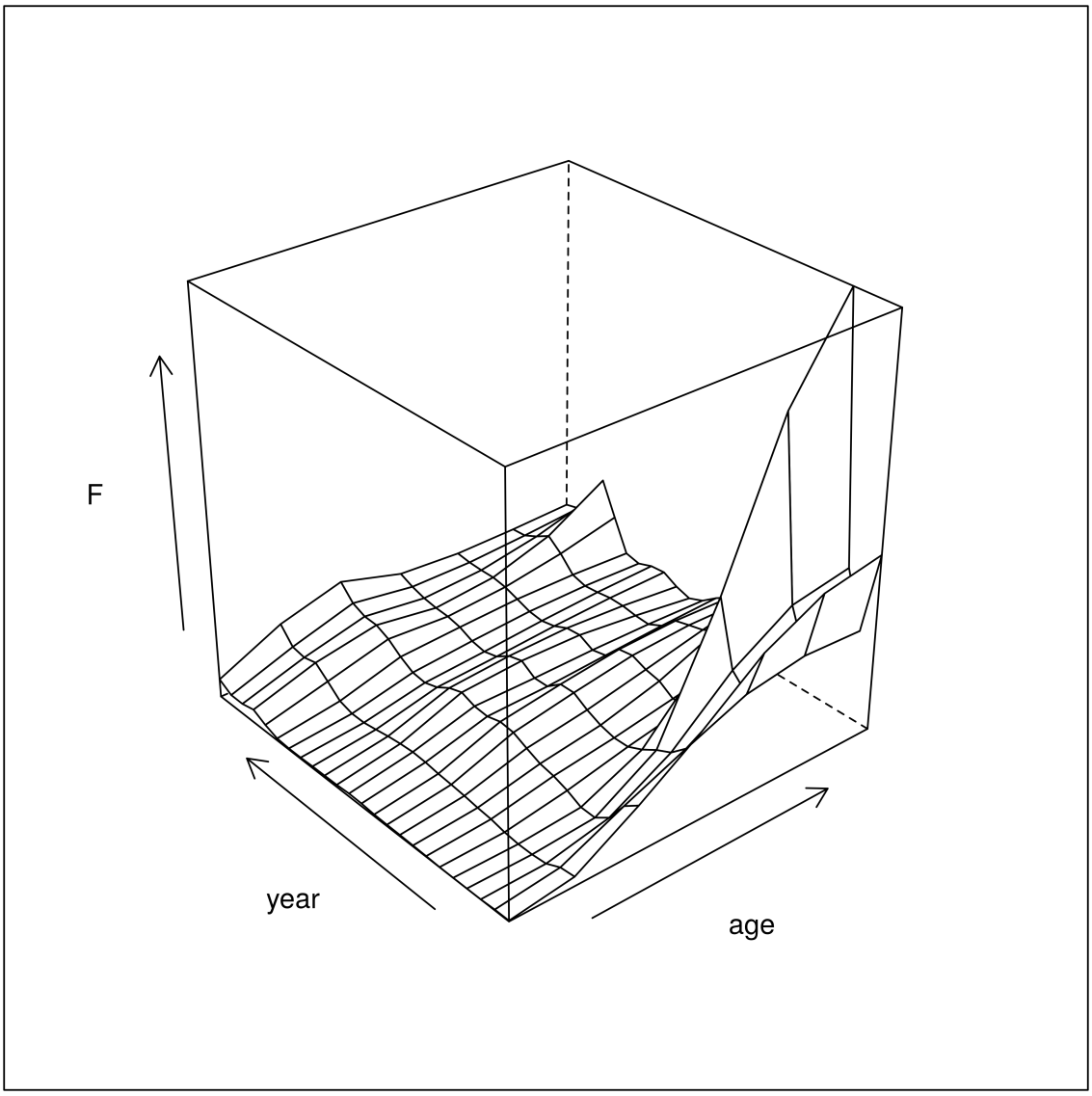

Figure 117: F-at-age estimate

```
plot(S.q2mc)
```

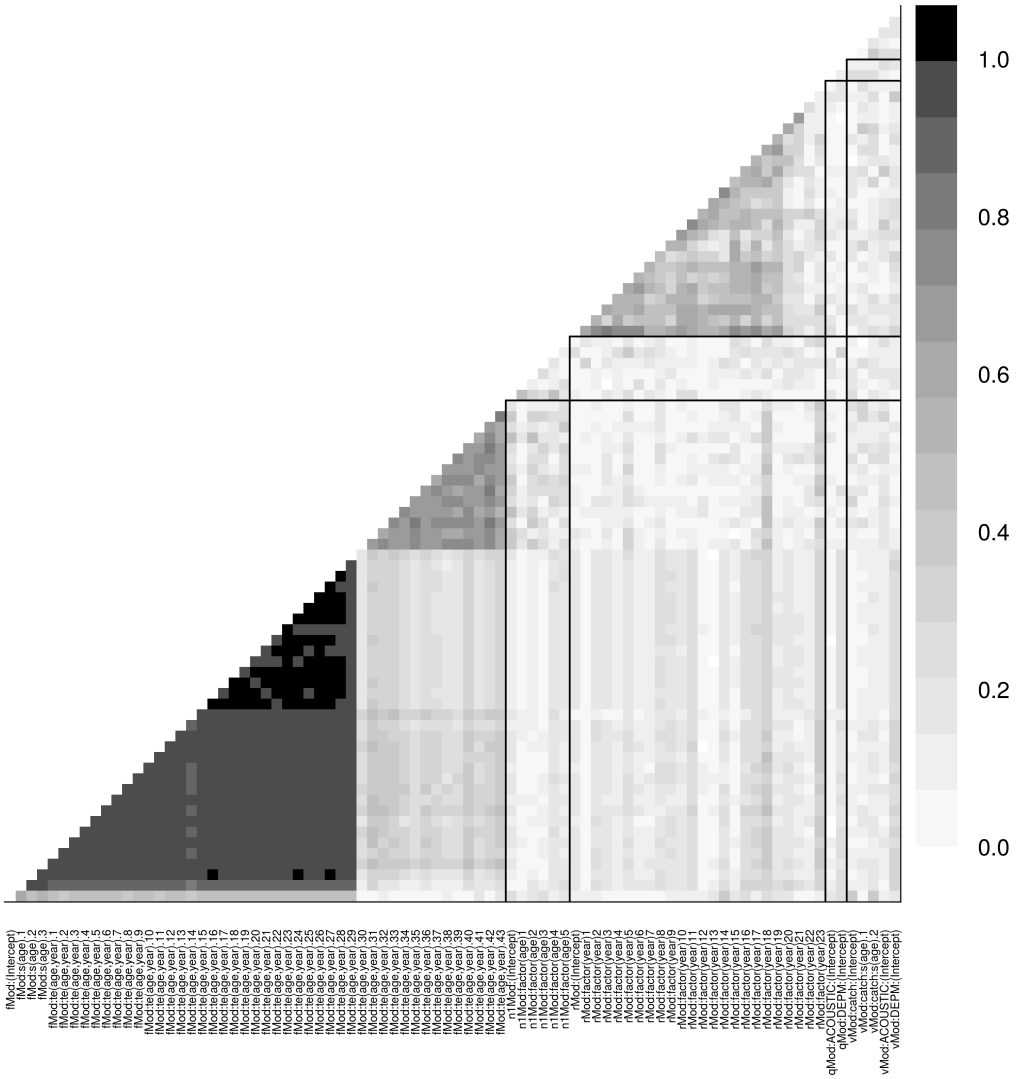

Figure 118: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(S.q2smc)
```

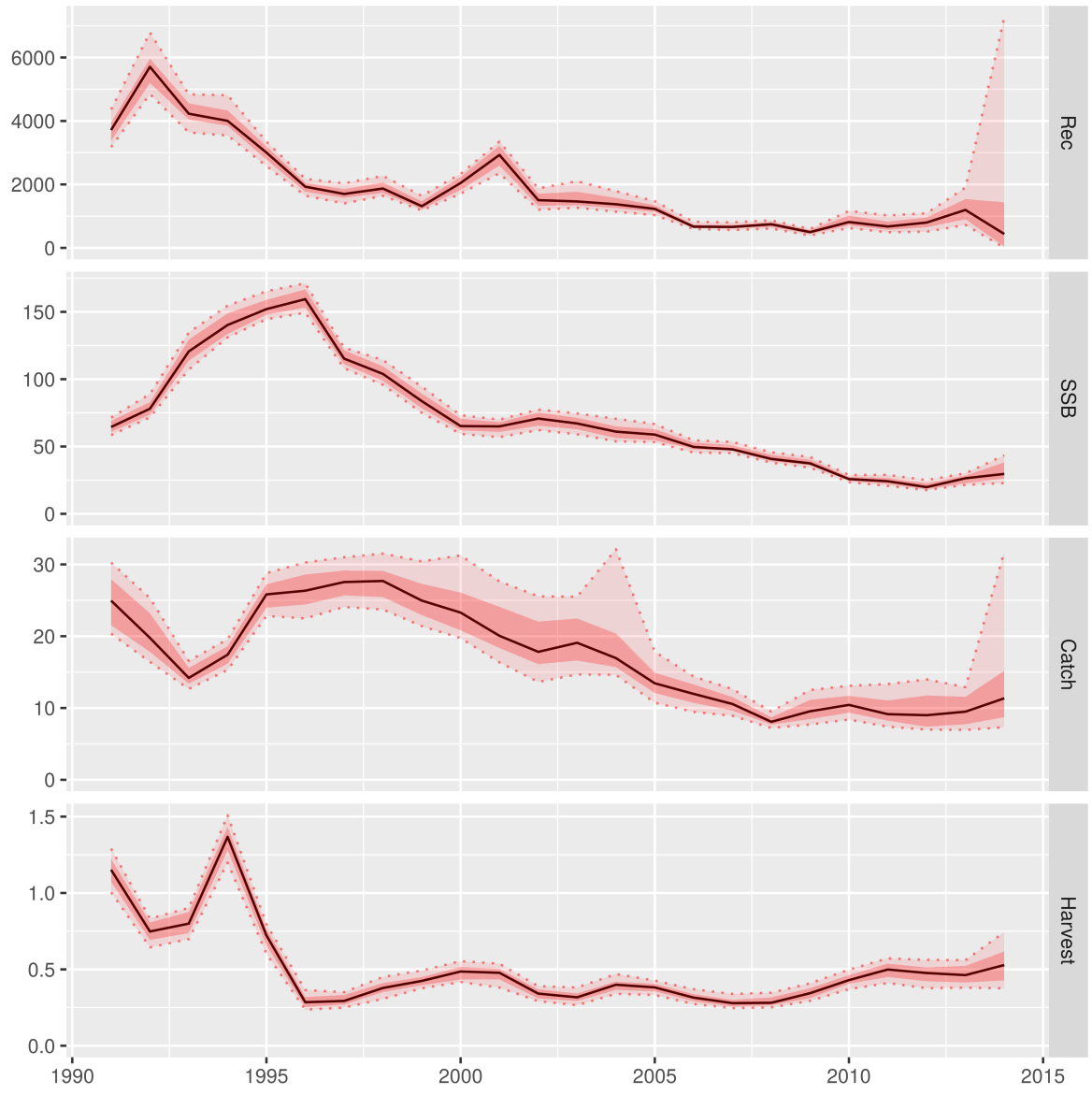

Figure 119: Summary plot

5.6.3 q option 3: smoother, survey overweighting

```
fmod <- ~s(age, k = 4) + te(age, year, k = c(3, 15))
qmod <- list(~s(age, k = 5), ~1)
S.idx2 <- S.idx
index.var(S.idx2[[1]]) <- 0.5
S.q3f <- a4aSCA(S.stk, S.idx2, fmodel = fmod, qmodel = qmod)
S.q3r <- residuals(S.q3f, S.stk, S.idx2)
S.q3s <- S.stk + simulate(S.q3f, 500)
S.q3mc <- a4aSCA(S.stk, S.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
S.q3mcmc <- as.mcmc(S.q3mc)
S.q3smc <- S.stk + S.q3mc
```

```
plot(S.q3r)
```

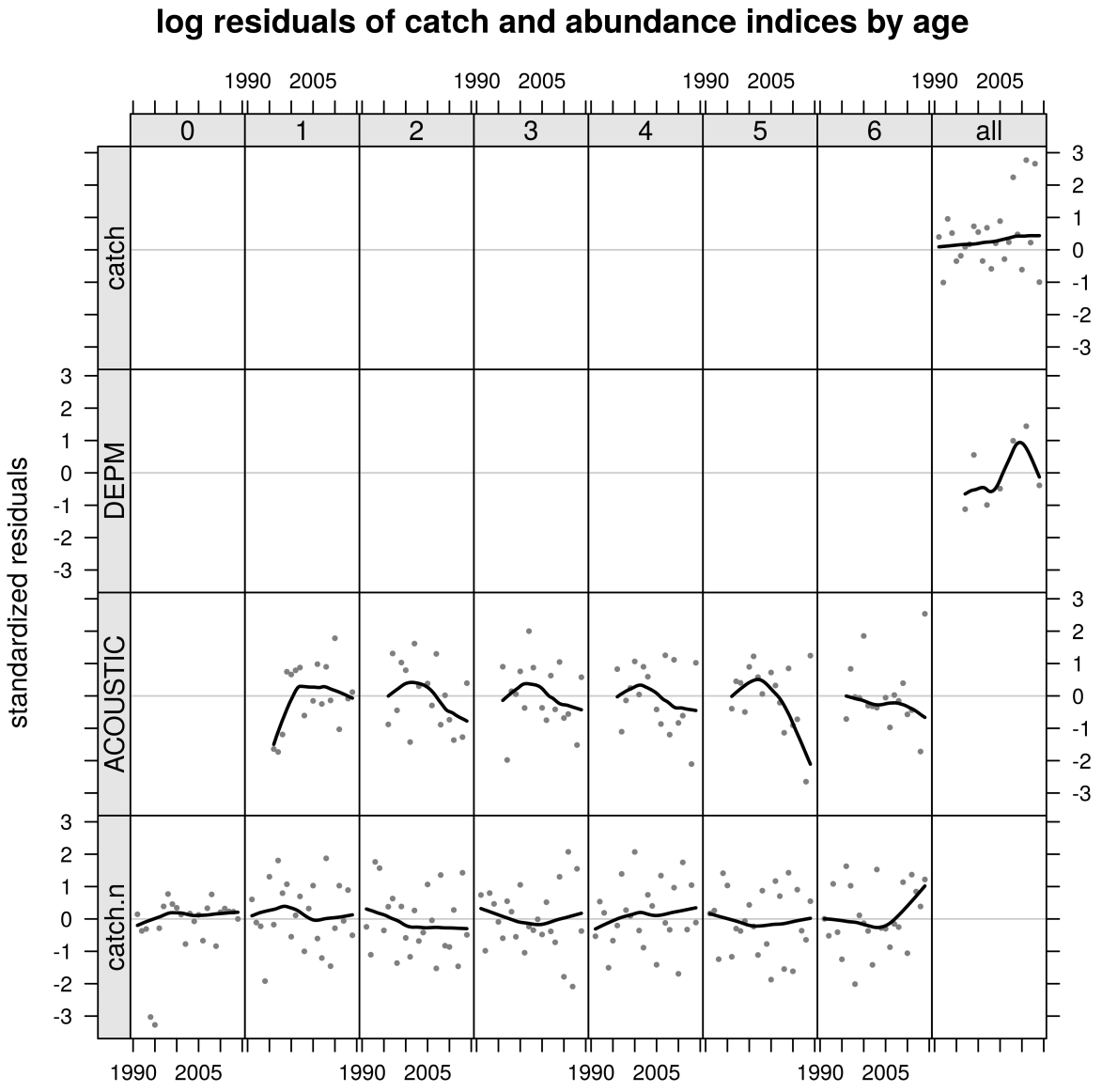

Figure 120: Residuals

```
plot(S.q3f, S.stk)
```

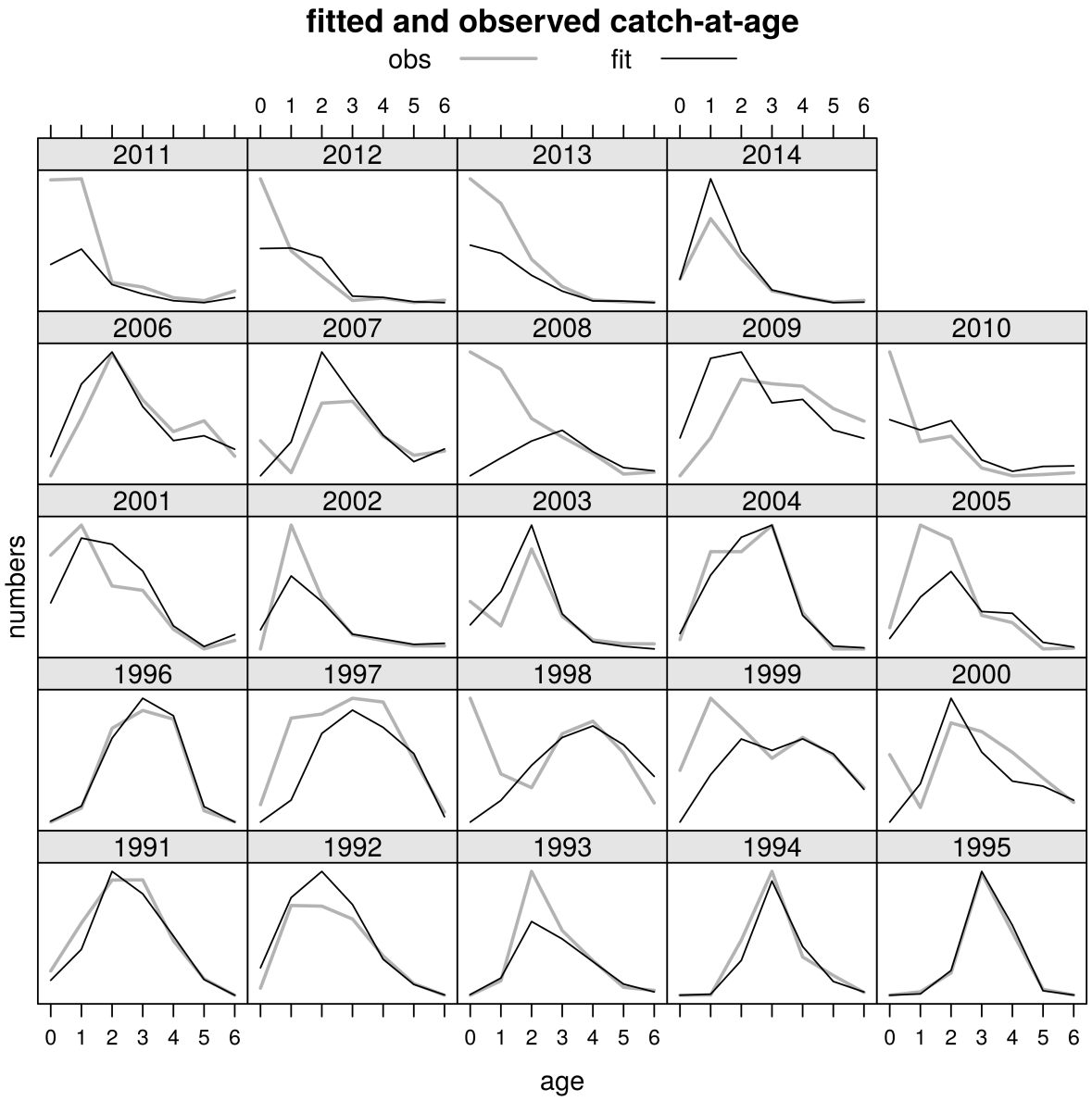

Figure 121: Catch-at-age predictions and observations

```
plot(S.q3f, S.idx2[1])
```

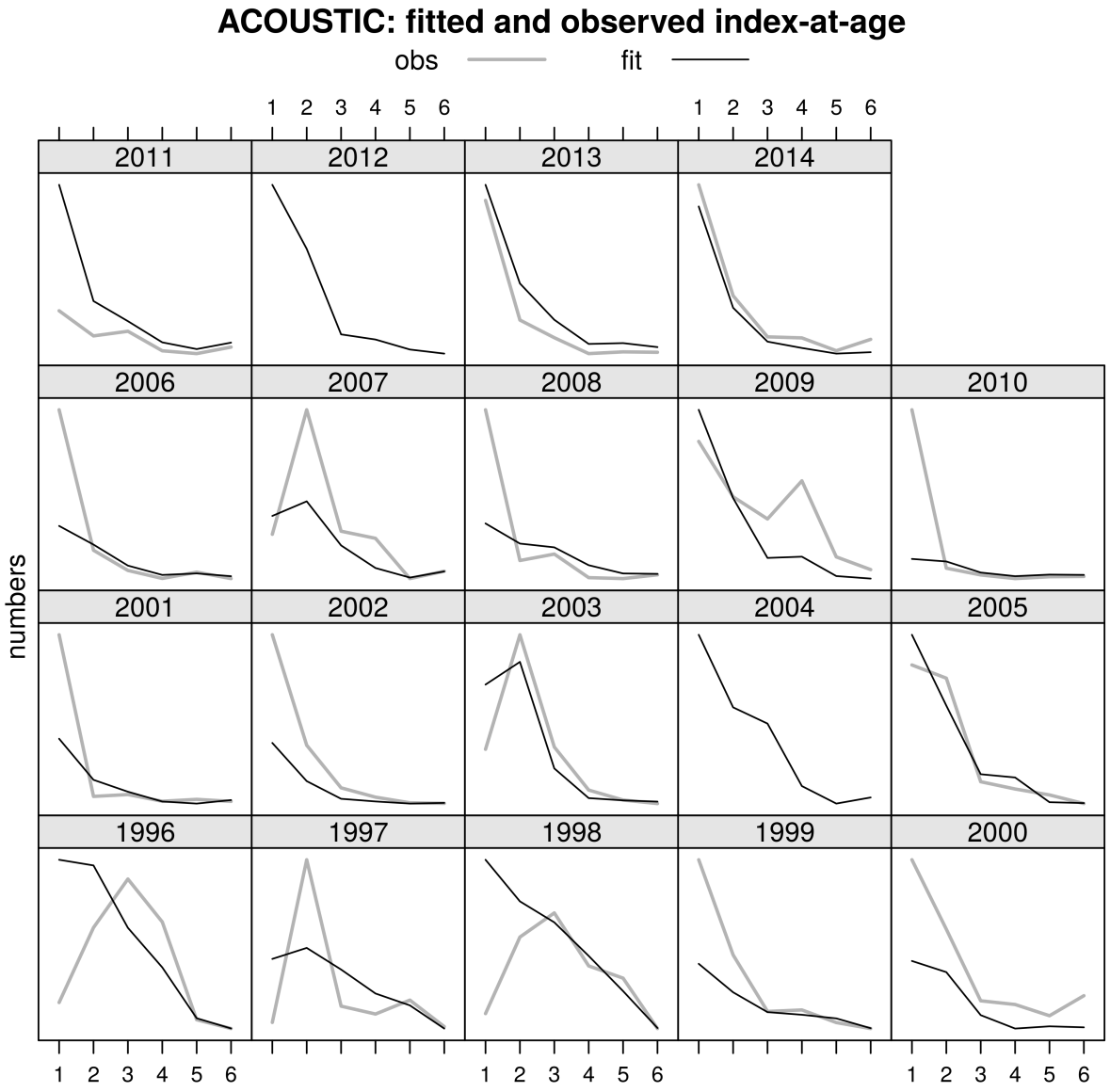

Figure 122: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(S.q3f))
```

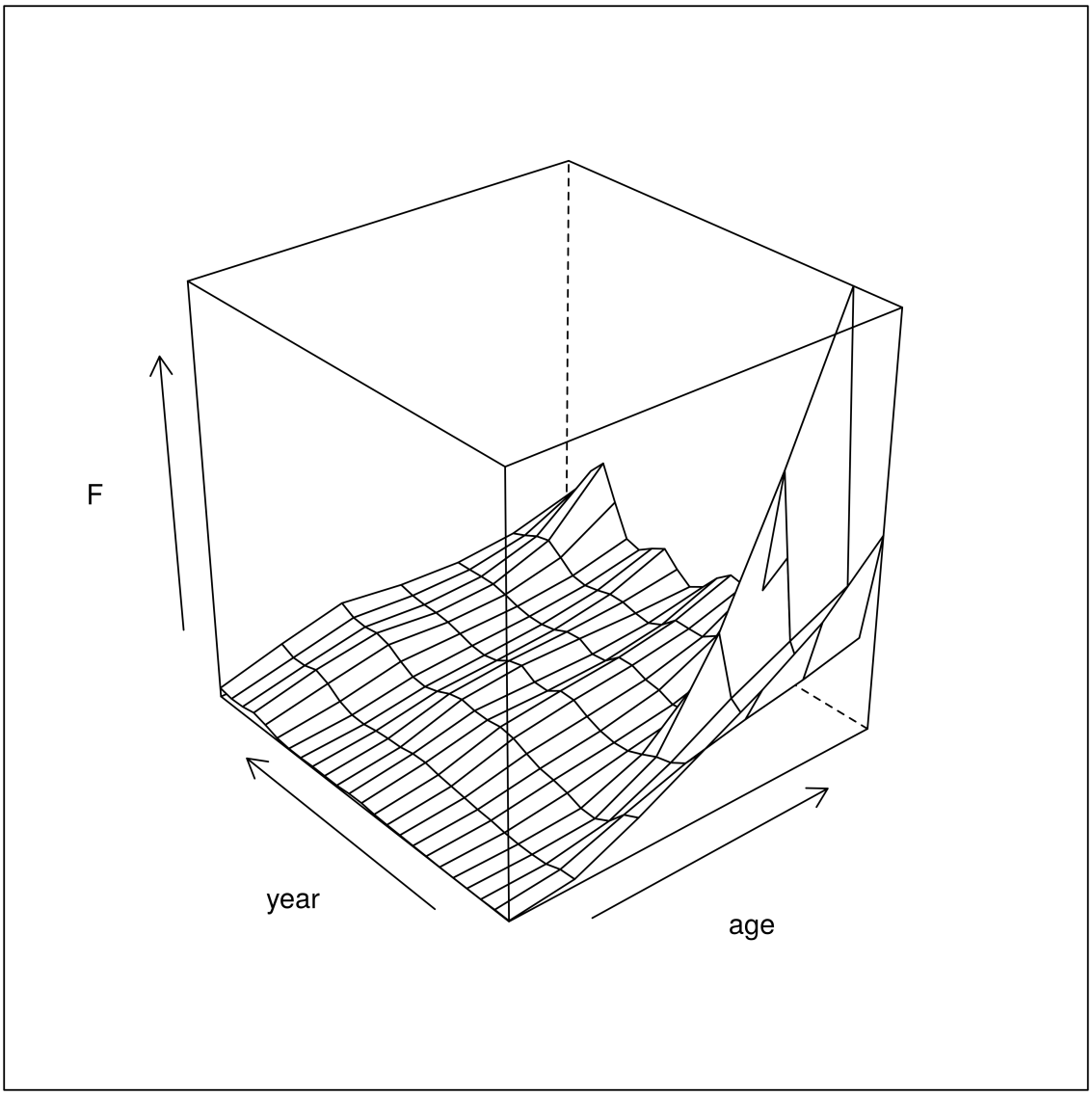

Figure 123: F-at-age estimate

```
plot(S.q3mc)
```

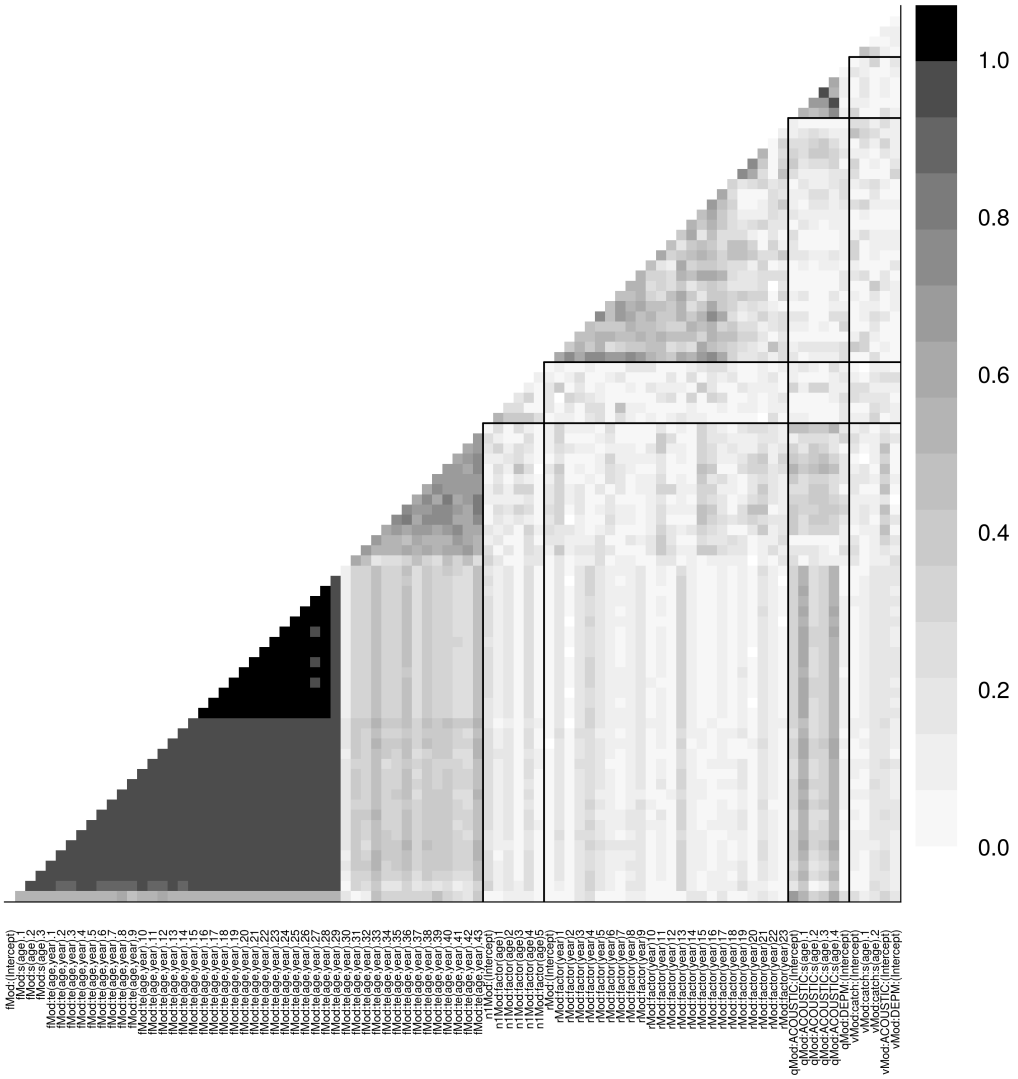

Figure 124: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(S.q3smc)
```

Figure 125: Summary plot

5.6.4 q option 4: constant, survey overweighting

```
fmod <- ~s(age, k = 4) + te(age, year, k = c(3, 15))
qmod <- list(~1, ~1)
S.idx2 <- S.idx
index.var(S.idx2[[1]]) <- 0.5
S.q4f <- a4aSCA(S.stk, S.idx2, fmodel = fmod, qmodel = qmod)
S.q4r <- residuals(S.q4f, S.stk, S.idx2)
S.q4s <- S.stk + simulate(S.q4f, 500)
S.q4mc <- a4aSCA(S.stk, S.idx2, fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
S.q4mcmc <- as.mcmc(S.q4mc)
S.q4smc <- S.stk + S.q4mc
```

```
plot(S.q4r)
```

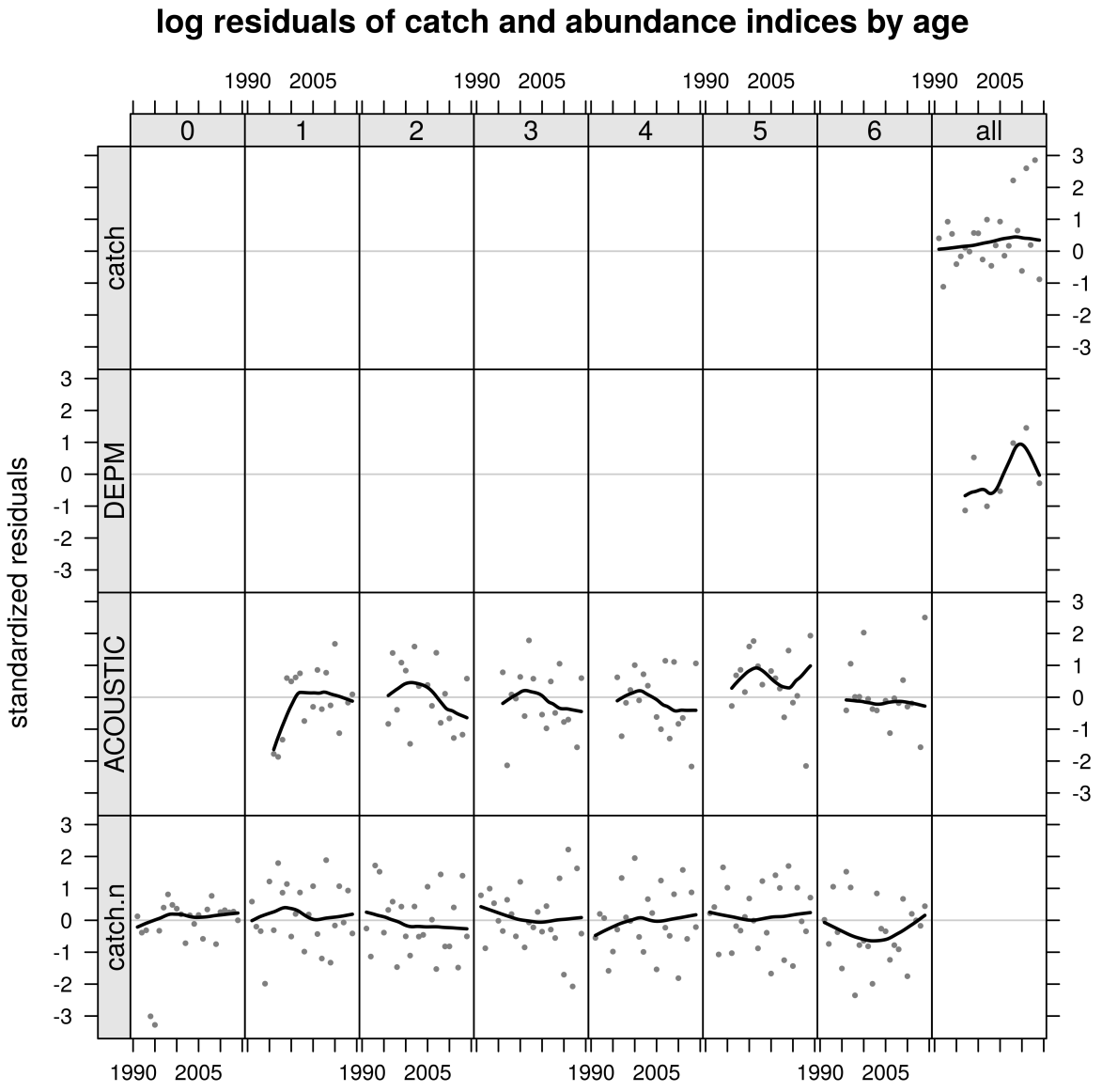

Figure 126: Residuals

```
plot(S.q4f, S.stk)
```

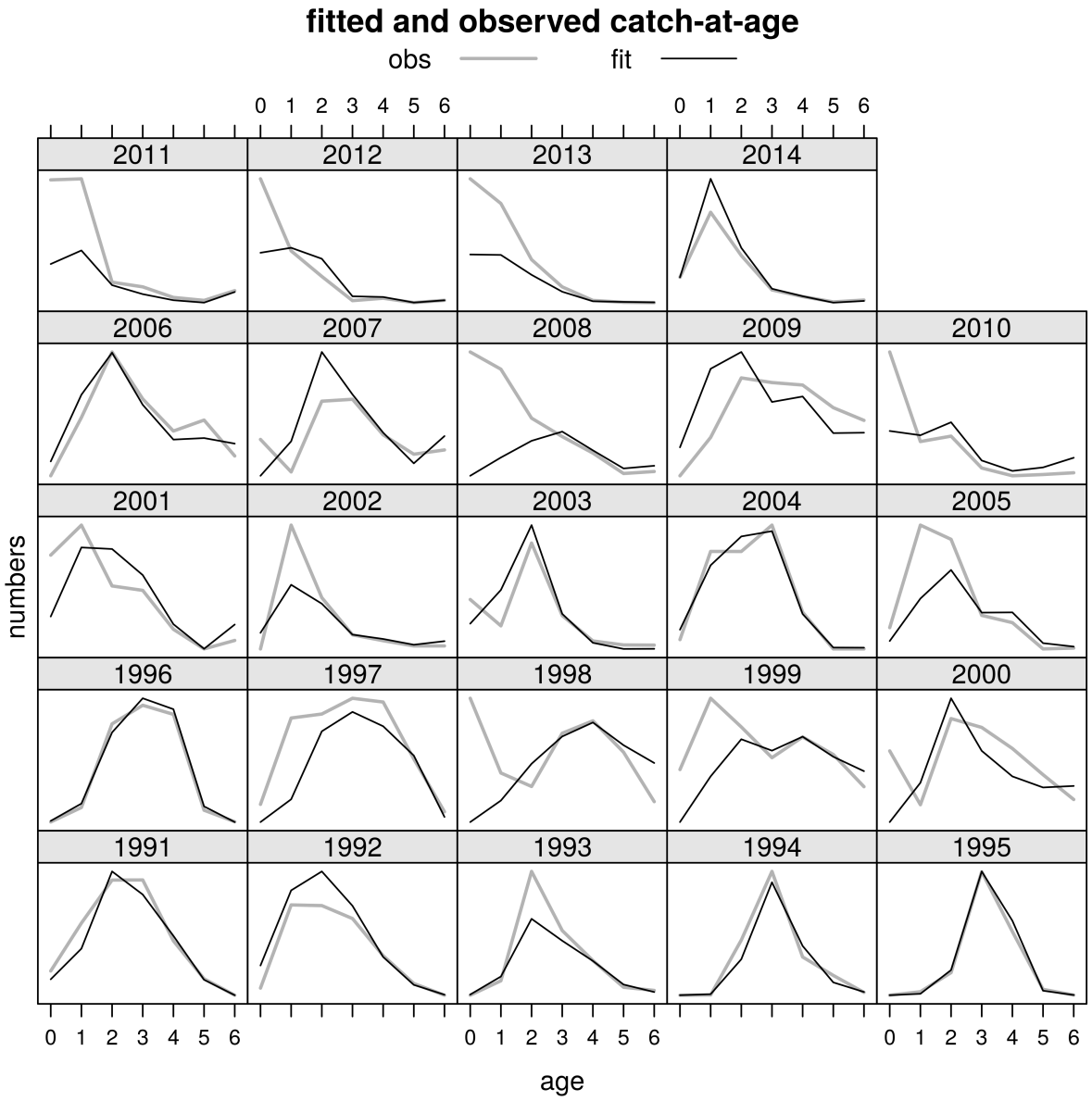

Figure 127: Catch-at-age predictions and observations

```
plot(S.q4f, S.idx2[1])
```

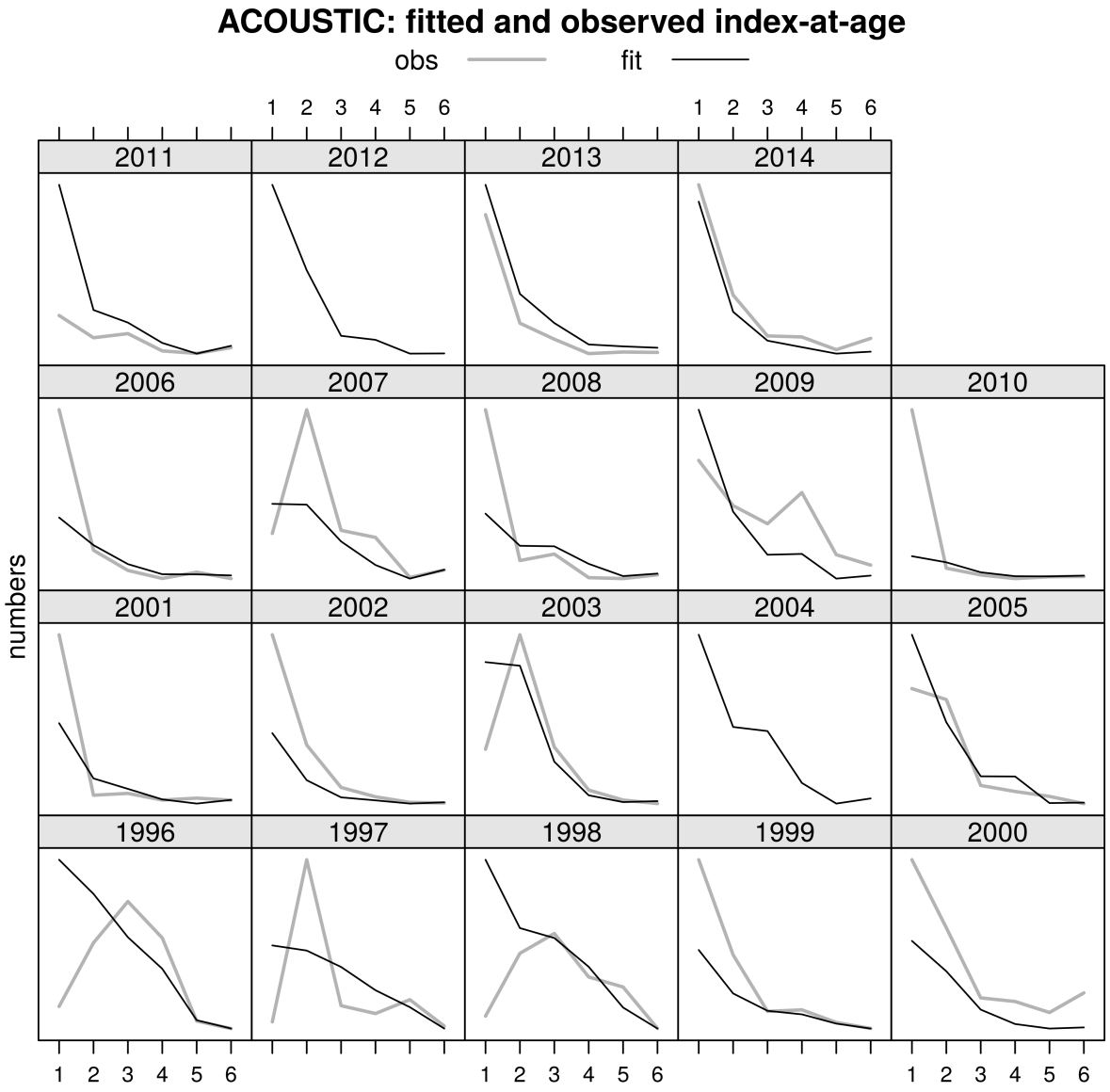

Figure 128: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(S.q4f))
```

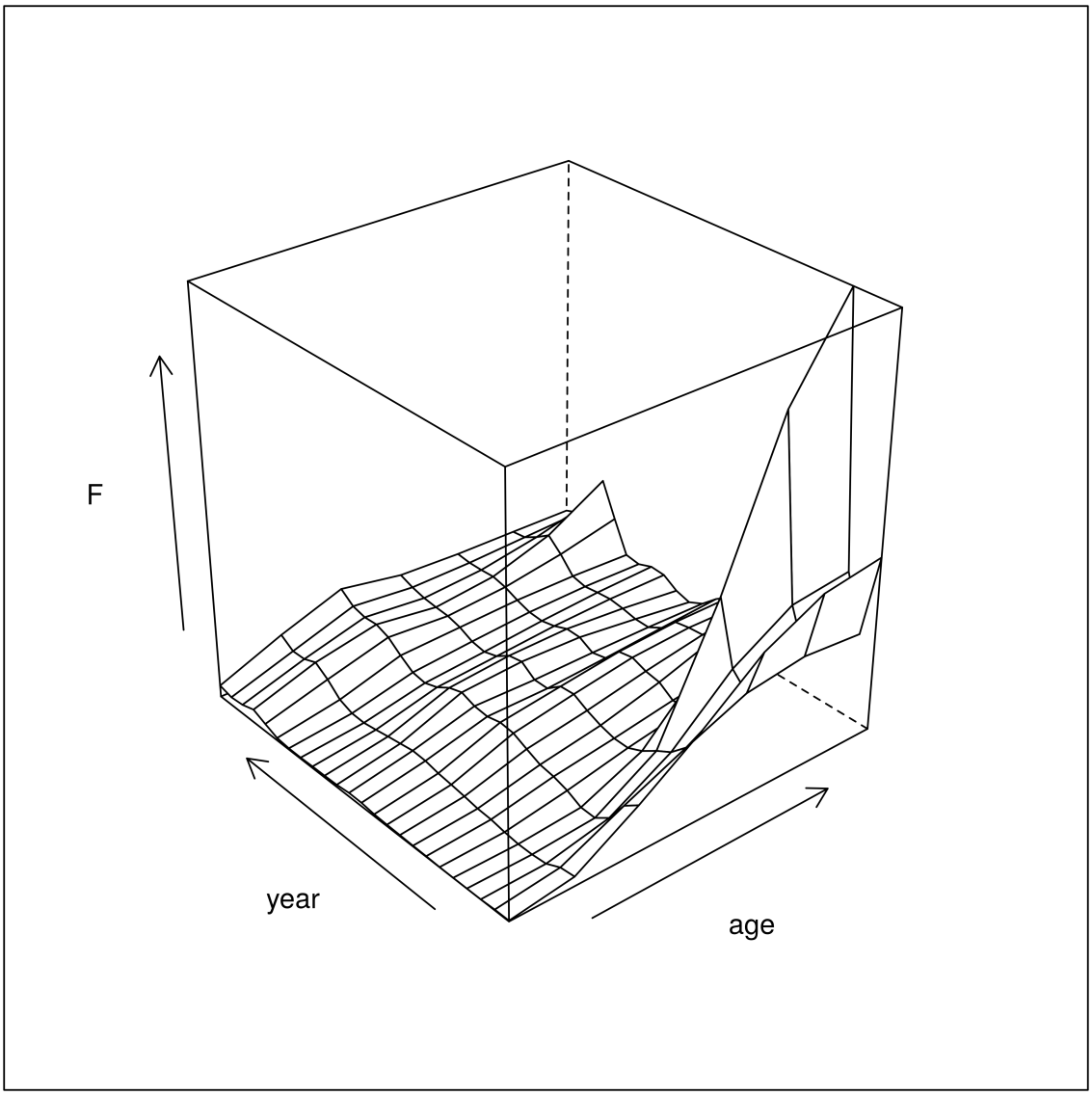

Figure 129: F-at-age estimate

```
plot(S.q4mc)
```

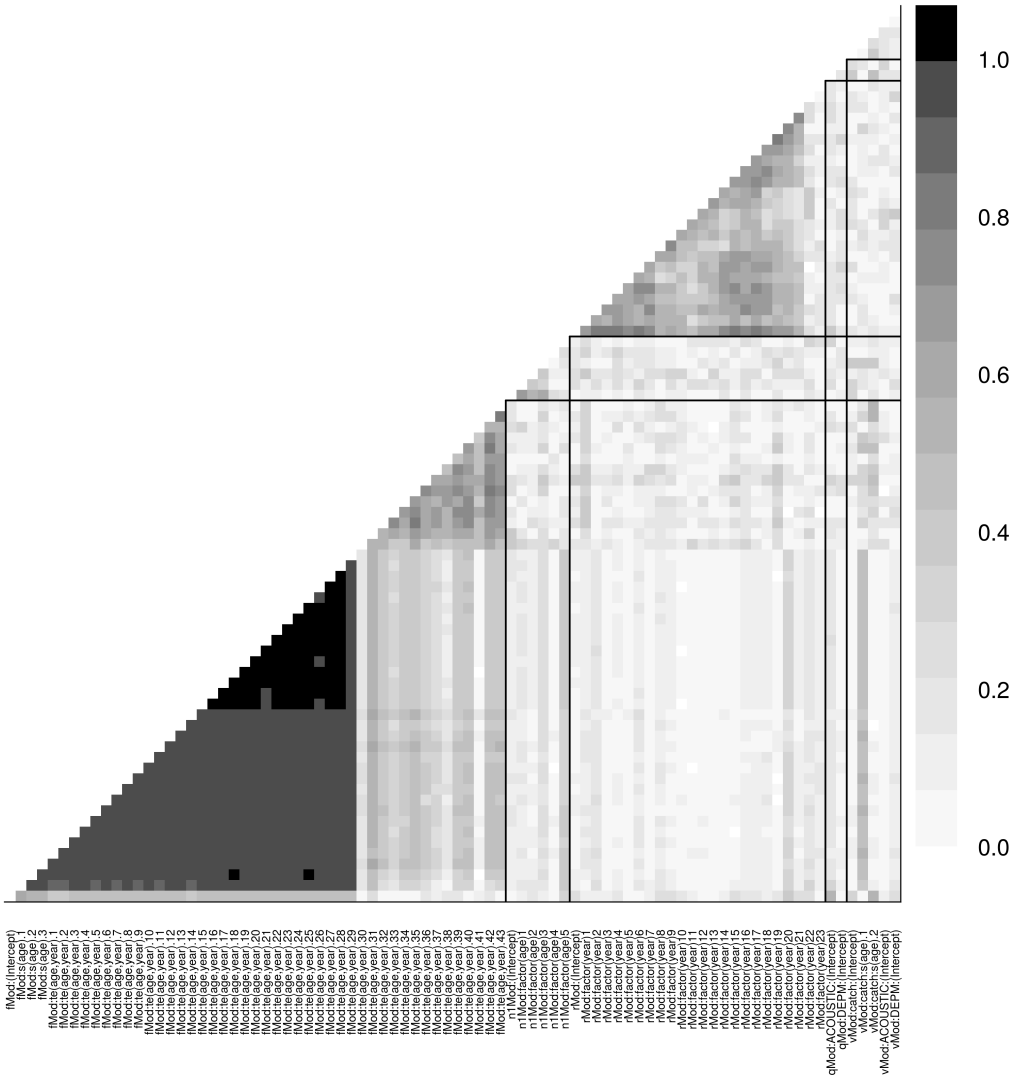

Figure 130: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(S.q4smc)
```

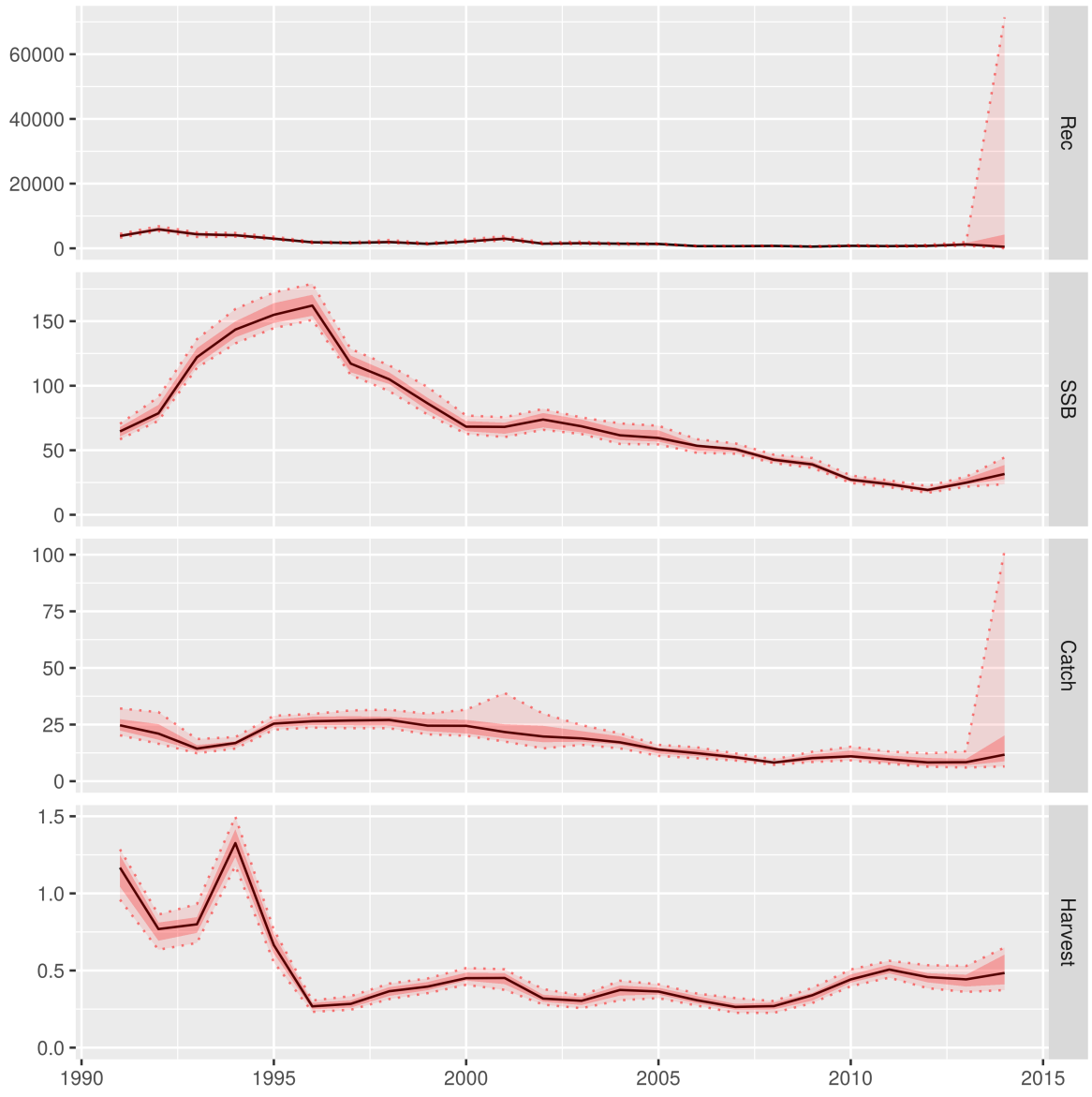

Figure 131: Summary plot

5.6.5 q option 5: constant, no overweighting of survey, no DEPM

```
fmod <- ~s(age, k = 4) + te(age, year, k = c(3, 15))
qmod <- list(~1)
S.q5f <- a4aSCA(S.stk, S.idx[1], fmodel = fmod, qmodel = qmod)
S.q5r <- residuals(S.q5f, S.stk, S.idx[1])
S.q5s <- S.stk + simulate(S.q5f, 500)
S.q5mc <- a4aSCA(S.stk, S.idx[1], fmodel = fmod, qmodel = qmod,
    fit = "MCMC", mcmc = SCAMCMC(mcmc = 12500, mcsave = 250,
        mcprobe = 0.4))
S.q5mcmc <- as.mcmc(S.q5mc)
S.q5smc <- S.stk + S.q5mc
```

```
plot(S.q5r)
```

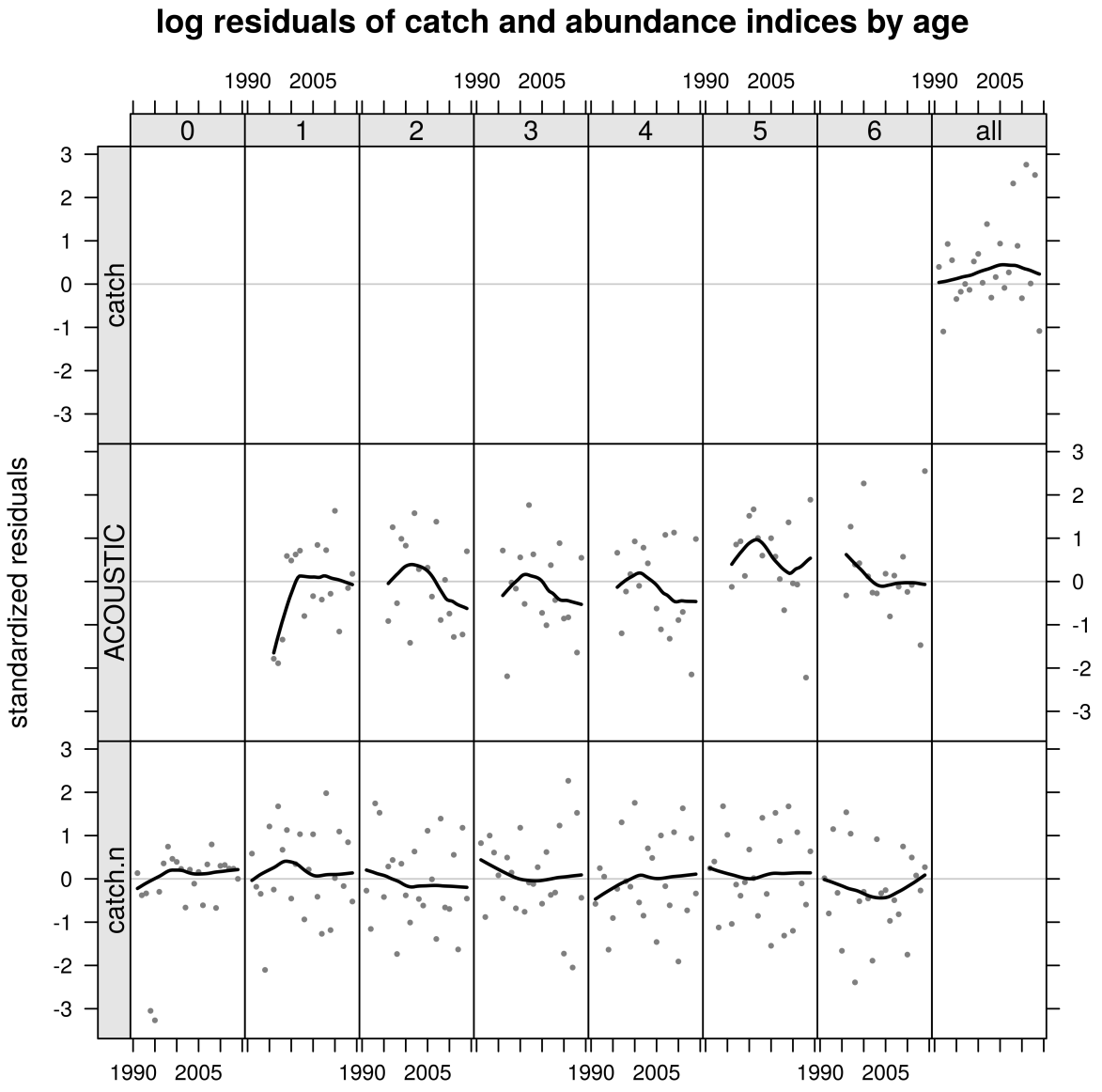

Figure 132: Residuals

```
plot(S.q5f, S.stk)
```

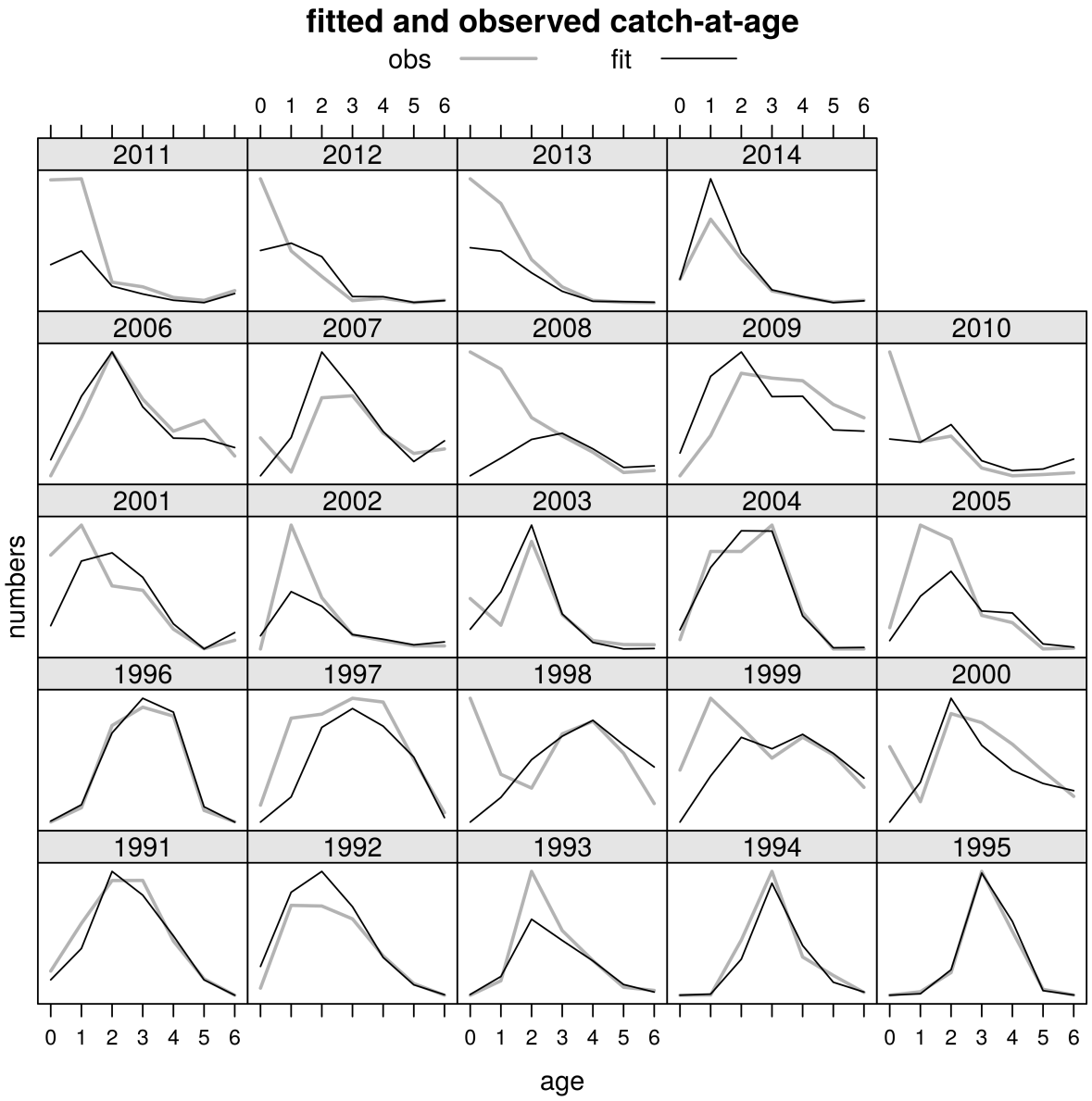

Figure 133: Catch-at-age predictions and observations

```
plot(S.q5f, S.idx[1])
```

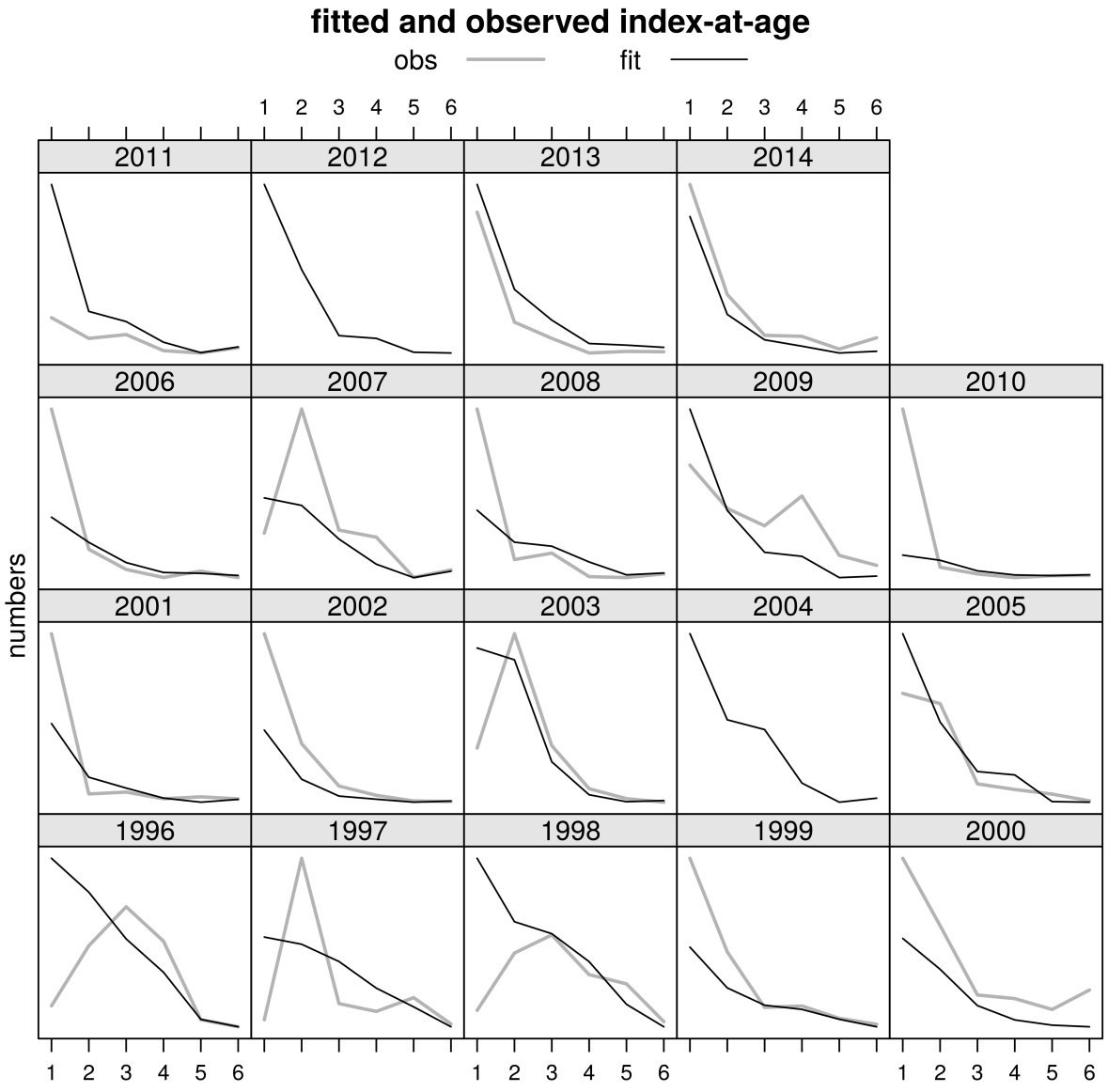

Figure 134: Index-at-age predictions and observations

```
wireframe(data ~ age + year, zlab = "F", data = harvest(S.q5f))
```

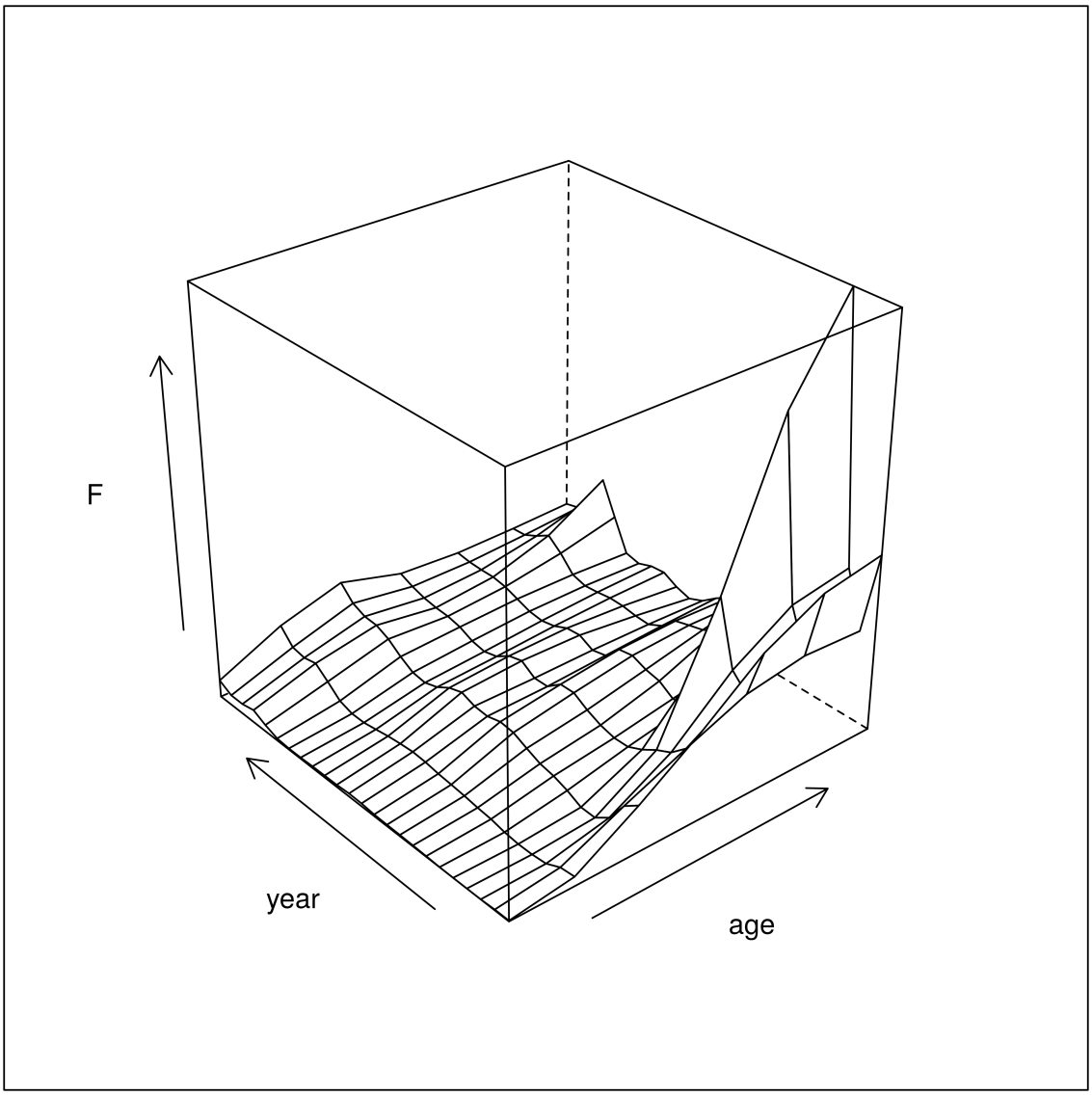

Figure 135: F-at-age estimate

```
plot(S.q5mc)
```

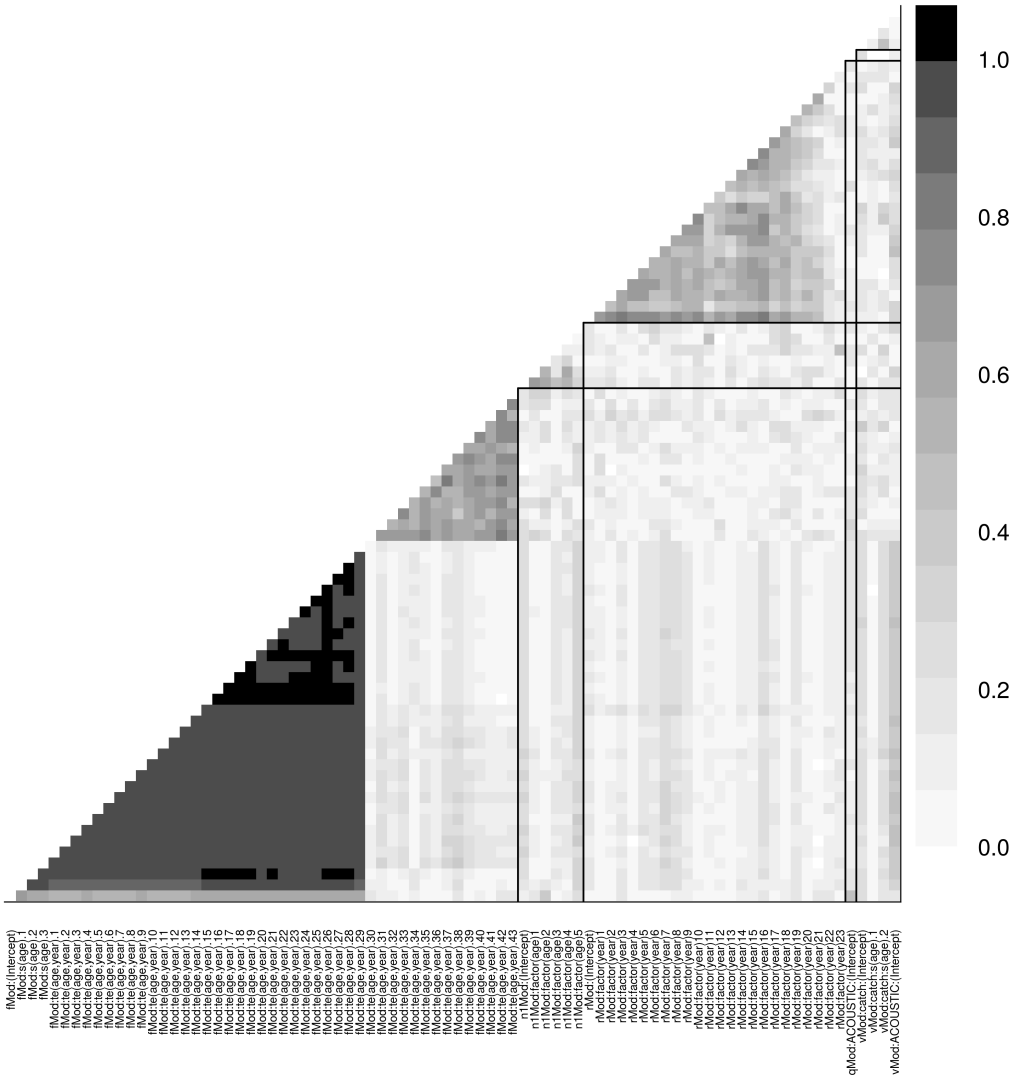

Figure 136: Absolute correlation between pairs of parameters. The blocks identify submodels and their interaction. Triangles refere to correlation between parameters of the same submodel, while rectangles refer to correlation between parameters of distinct sub-models

```
plot(S.q5smc)
```

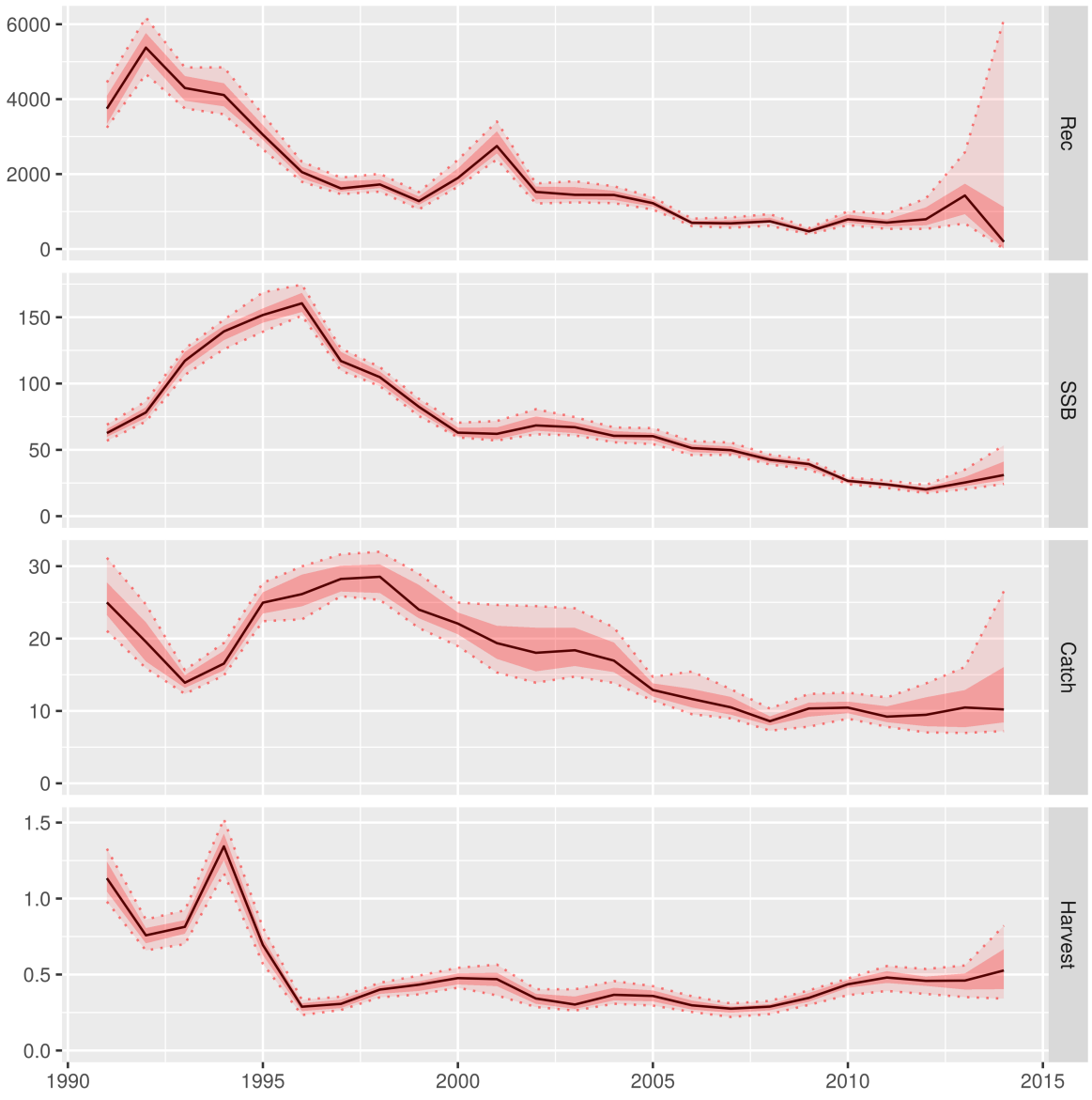

Figure 137: Summary plot

5.6.6 Comparison across assessments

```
plot(FLStocks(q1 = S.q1smc, q2 = S.q2smc, q3 = S.q3smc, q4 = S.q4smc,
    q5 = S.q5smc))
```

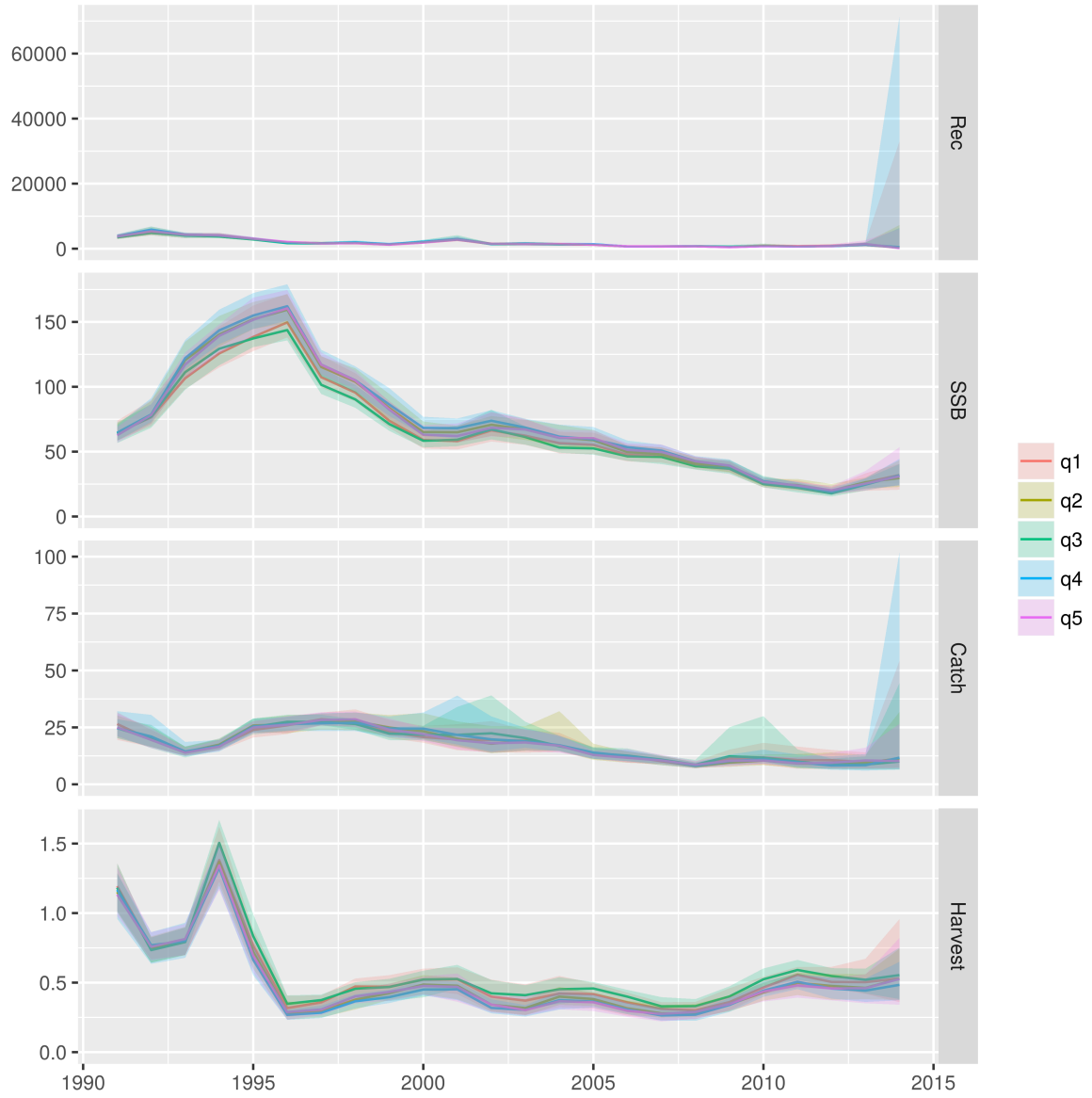

Figure 138: All assessments summary

6. Replicating the FLa4a separable model with JAGS

```
load("../analysis/JAGS/V1objects.RData")
```

For the BB case study, a bayesian approach has also been implemented. In order to compare both methods (a4a and bayesian) a very simple model have been selected: a separable submodel for fishing mortality using factors for year and age, constant catchability for both surveys, constant variance for each observation process, a year factor for recruitment and an age factor for first year abundance estimates.

In the a4a approach, we define this model by specifing:

- fmodel <- ~ factor(year) + factor(age) - 1
- qmodel <- list(~1, ~1)
- vmodel <- list(~1, ~1, ~1)
- srmodel <- ~ factor(year)
- n1model <- ~ factor(age)

Inside the a4a framework two different types of results have been computed for comparison:

1. Simulations using maximum likelihood results and a multivariate normal distribution (with the variance-covariance matrix from the hessian)
2. Using the MCMC option, where starting from maximum likelihood results the Metropolis-Hastings algorithm is implemented.

For the Bayesian approach prior distributions have been defined for all unknown parameters. Lognormal distributions have been used as priors in all cases except for precision parameters for which gamma distributions were chosen. The model is programed in Jags and run via R using R2jags package. Some results have been transformed and saved as FLR object for an easier comparison with a4a output.

2000 iterations have been saved in all runs using a thinning of 200 for a4a MCMC run and a thinning of 100 for the Bayesian run. Regarding autocorrelation and trace plots no problems were detected in any of the cases.

In the summary plot of the three runs similar tendencies are observed. However, some estimates and variability may differ, mainly for last years.

```
plot(FLStocks(Bayesian = BB.stk + Bayes.fit, MCa4a = BB.stk +
    a4a.MC, SIMa4a = BB.stk + a4a.SIM))
```

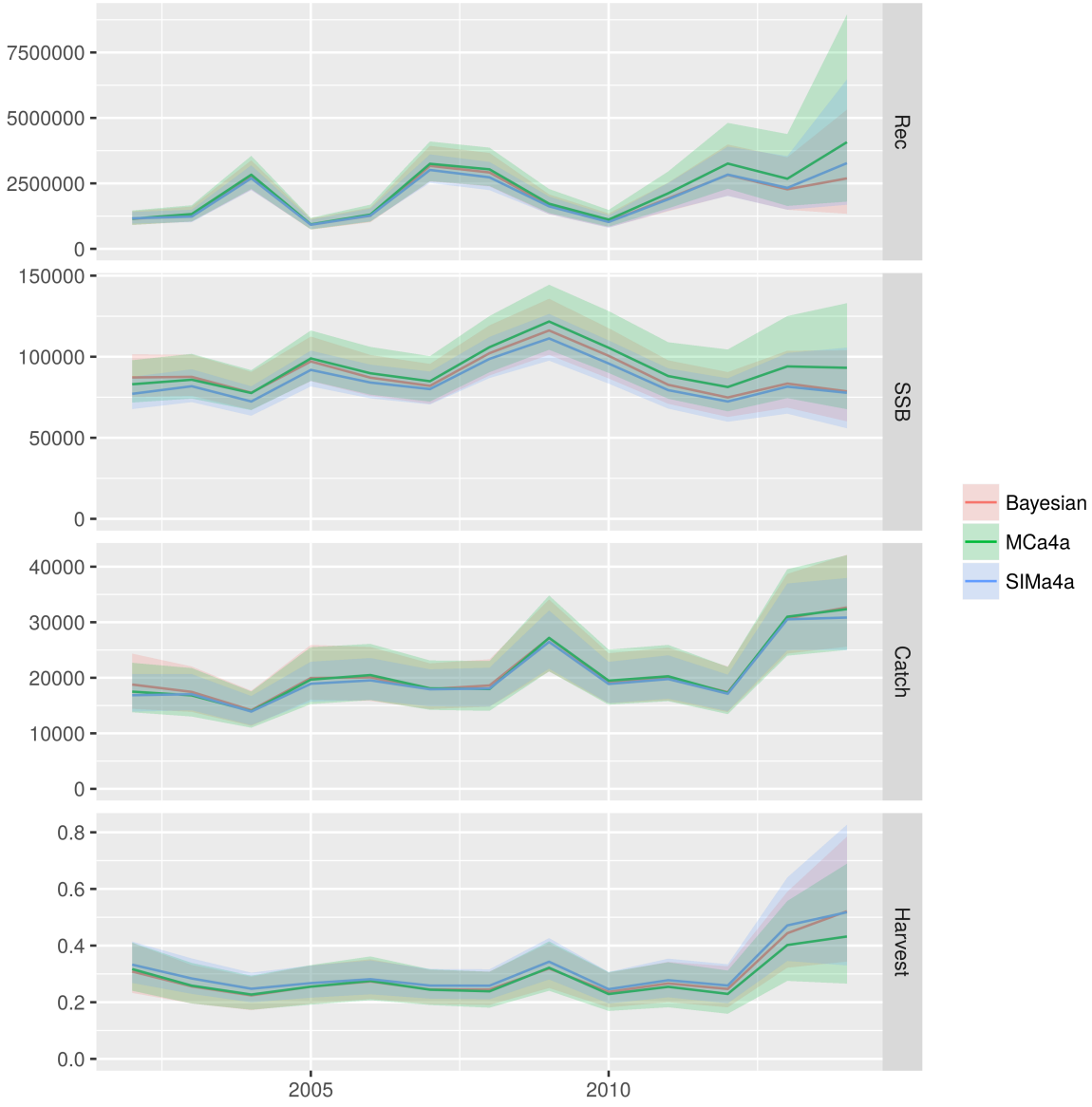

Figure 139: Fits with a4a stochastic simulation, a4a MCMC and JAGS separable model.

The following plots show the variance among interations for each estimate (computed using iterVars). Variability in a4a SIM run appears to be lower fishing mortality, catch and stock estimates, except for last year and last age of fishing mortality. On the other hand, a4a MCMC run estimates have higher variability. For the index estimates the a4a SIM run presents more variability.

```
Fvar <- FLQuants(Byes_F = iterVars(harvest(Bayes.fit)), a4aMC_F = iterVars(harvest(a4a.MC)),
    a4aSIM_F = iterVars(harvest(a4a.SIM)))
Nvar <- FLQuants(Byes_N = iterVars(stock.n(Bayes.fit)), a4aMC_N = iterVars(stock.n(a4a.MC)),
    a4aSIM_N = iterVars(stock.n(a4a.SIM)))
Cvar <- FLQuants(Byes_C = iterVars(catch.n(Bayes.fit)), a4aMC_C = iterVars(catch.n(a4a.MC)),
    a4aSIM_C = iterVars(catch.n(a4a.SIM)))
Iacvar <- FLQuants(Byes_C = iterVars(index(Bayes.fit)[[1]]),
    a4aMC_C = iterVars(index(a4a.MC)[[1]]), a4aSIM_C = iterVars(index(a4a.SIM)[[1]]))
```

```
xyplot(data ~ year | age, groups = qname, data = Fvar, type = "b",
    scales = "free", pch = 16, auto.key = list(title = "F iter variance",
        space = "top", cex = 0.8))
```

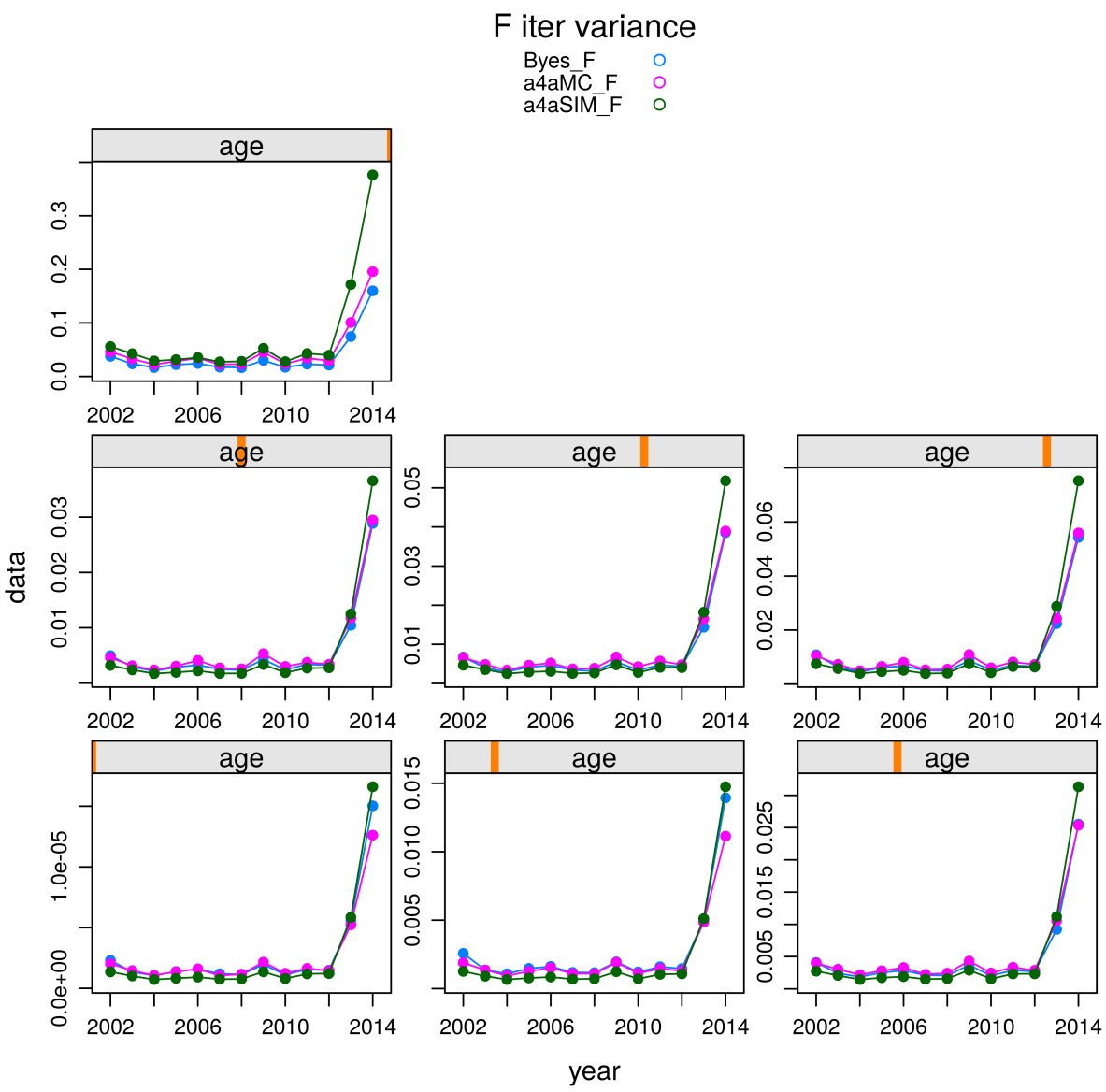

Figure 140: Variability across iterations of fishing mortality estimates by method

```
xyplot(data ~ year | age, groups = qname, data = Nvar, type = "b",
    scales = "free", pch = 16, auto.key = list(title = "N iter variance",
        space = "top", cex = 0.8))
```

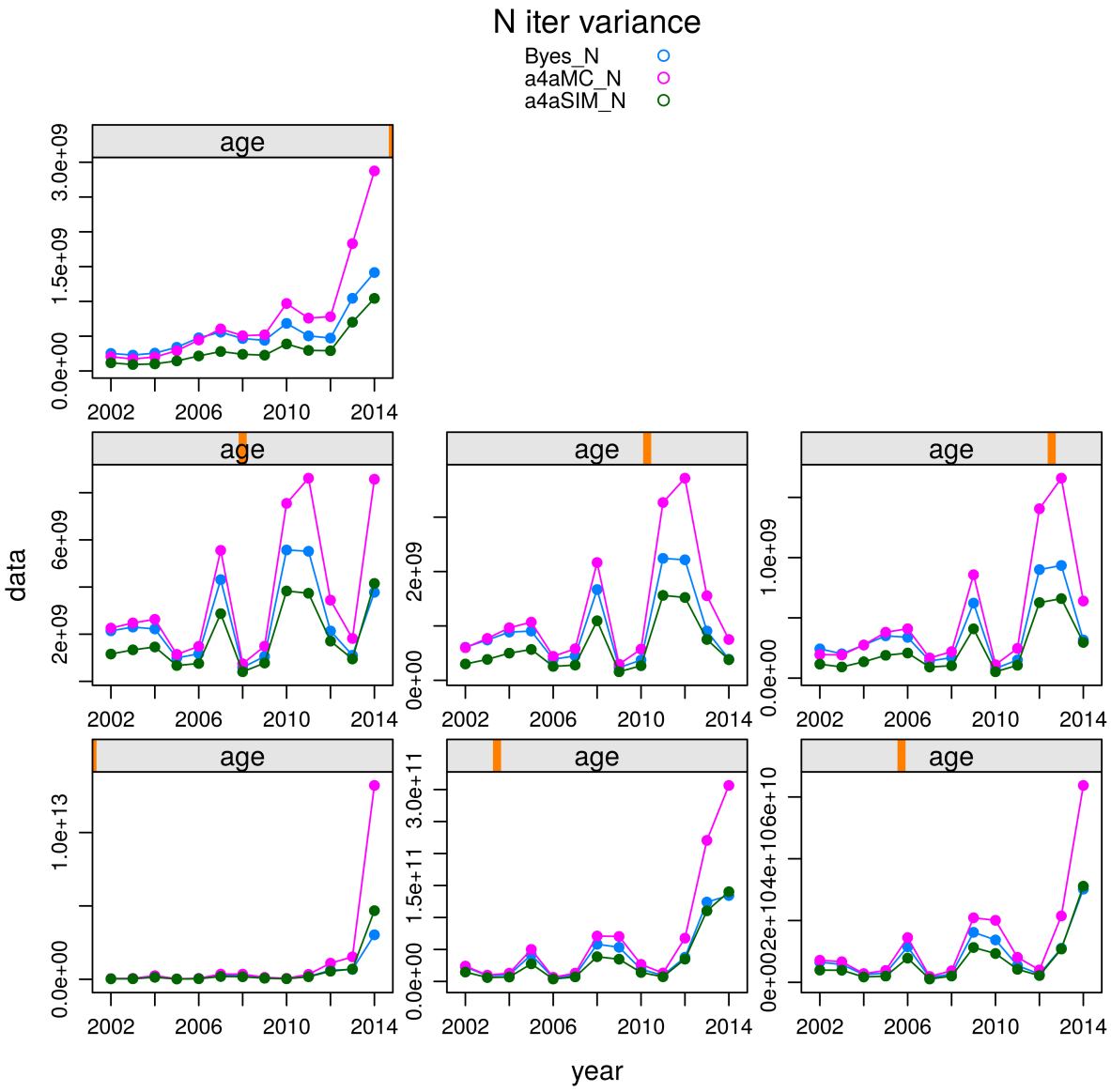

Figure 141: Variability across iterations of population abundance estimates by method

```
xyplot(data ~ year | age, groups = qname, data = Cvar, type = "b",
    scales = "free", pch = 16, auto.key = list(title = "Catch iter variance",
        space = "top", cex = 0.8))
```

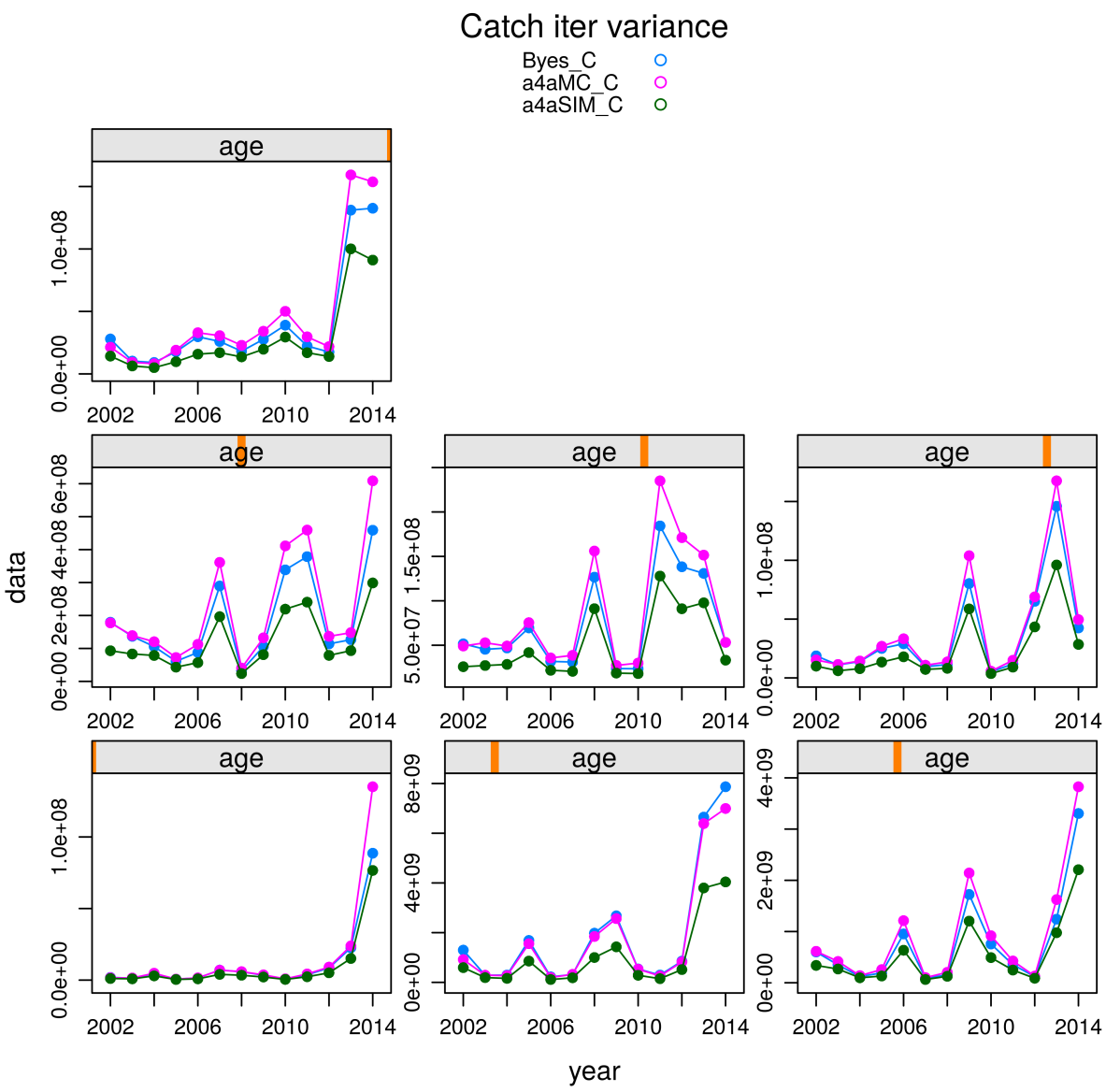

Figure 142: Variability across iterations of catches at age estimates by method

```
xyplot(data ~ year | age, groups = qname, data = Iacvar, type = "b",
    scales = "free", pch = 16, auto.key = list(title = "Acoustic survey index iter variance",
        space = "top", cex = 0.8))
```

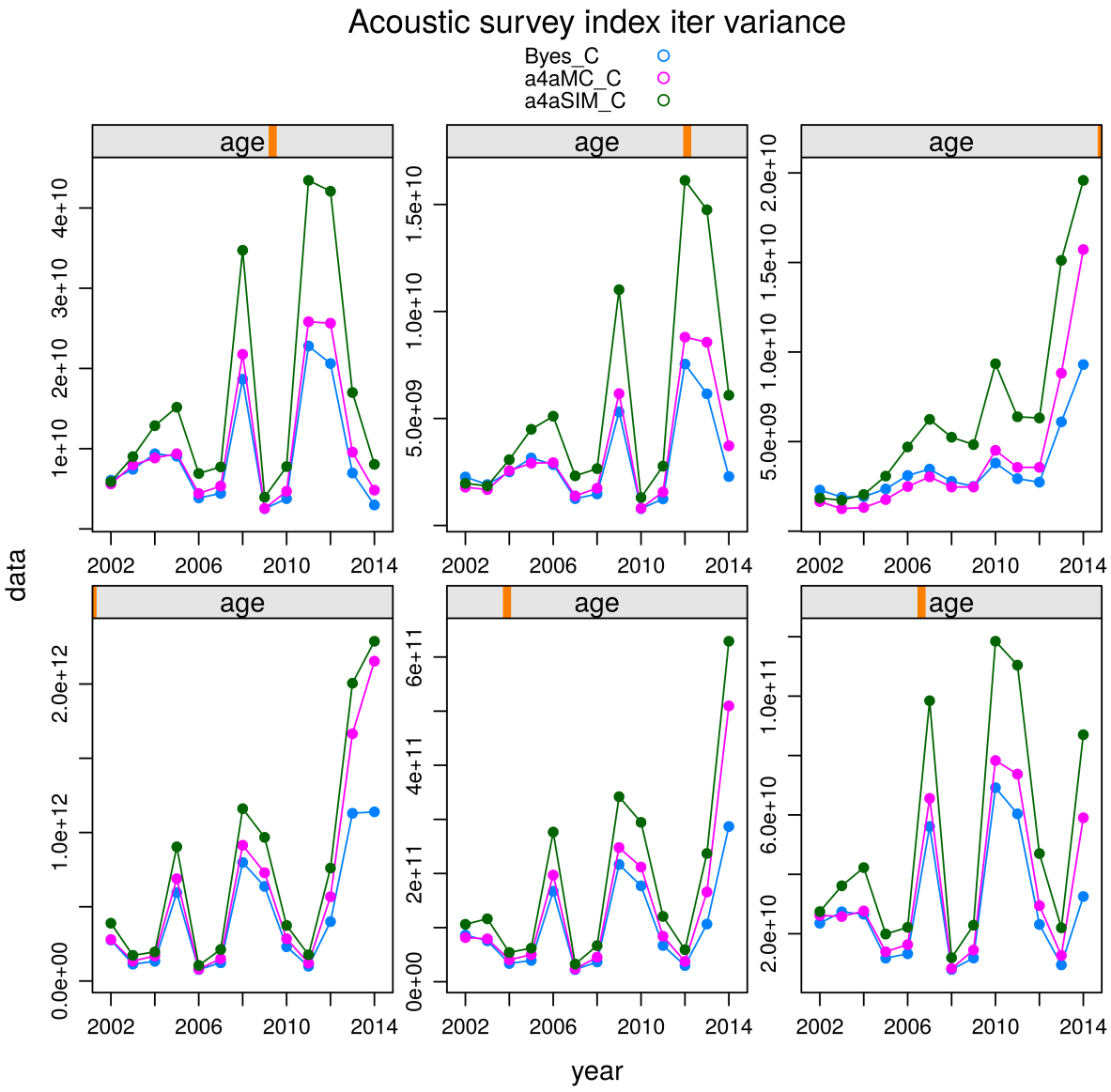

Figure 143: Variability across iterations of abundance indices estimates by method

Focusing on last year N variability and ploting the complete posterior distributions of centered estimations it can be seen that a4a MCMC run presents higher variability:

```
par(mfrow = c(2, 4))
for (j in 13:13) {
    for (i in 1:7) {
        plot(density(stock.n(Bayes.fit)[i, j, ] - iterMedians(stock.n(Bayes.fit)[i,
            j])), col = 2, main = paste("N 2014, age", i - 1),
            xlab = "centered N", lwd = 1)
        lines(density(stock.n(a4a.MC)[i, j, ] - iterMedians(stock.n(a4a.MC)[i,
            j])), col = 3, lwd = 1)
        lines(density(stock.n(a4a.SIM)[i, j, ] - iterMedians(stock.n(a4a.SIM)[i,
            j])), col = 4, lwd = 1)
        abline(v = 0)
        if (i == 1) {
            legend("topright", legend = (c("Bayes", "a4aMC",
                "a4aSIM")), lty = 1, col = c(2:4), cex = 2)
        }
    }
}
```

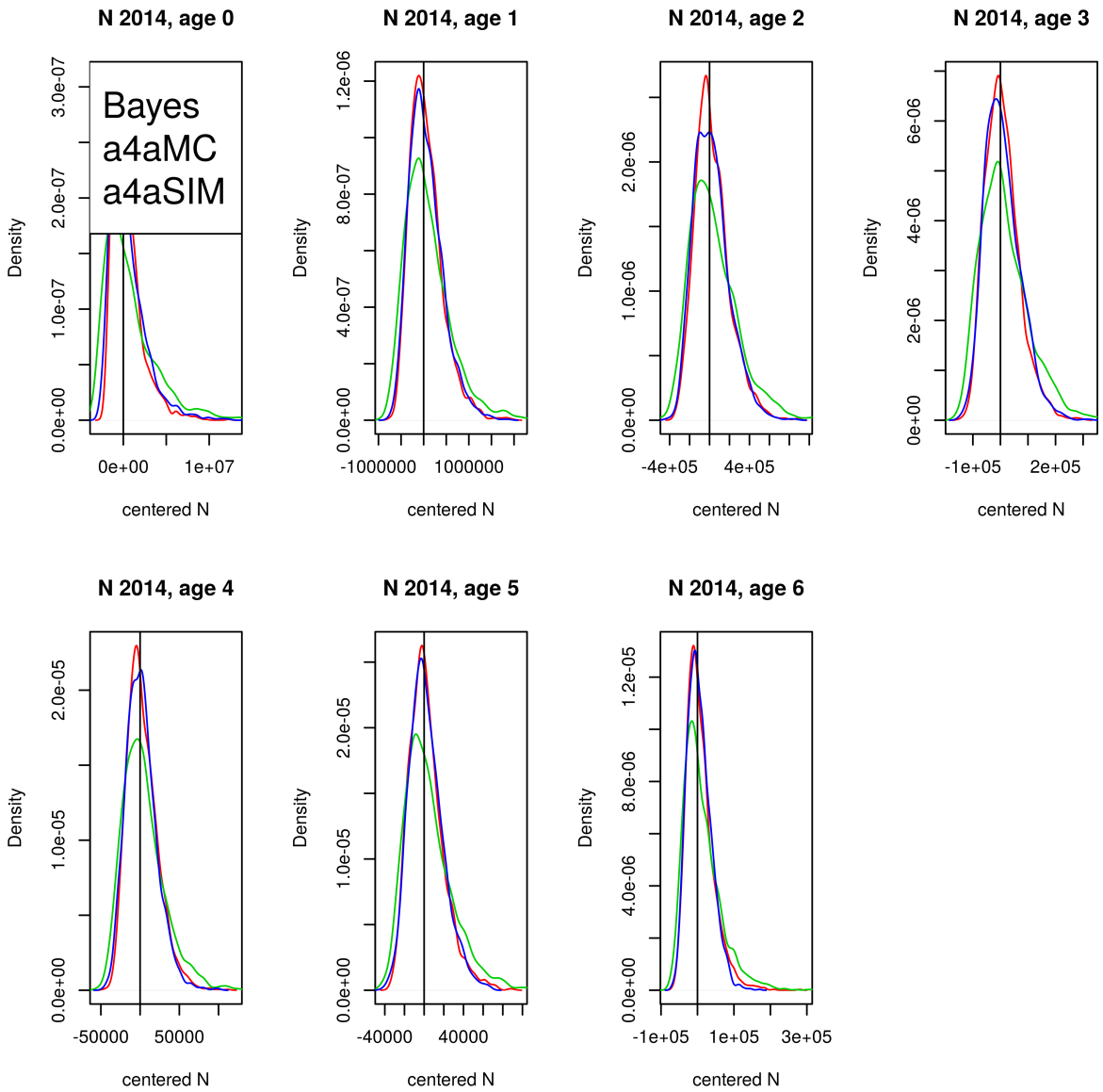

Figure 144: Variability of final year's estimates of population abundance by method

Other model parameters, fishing mortality age and year effect, catchability and variance parameters have been also compared. In the Bayesian run, fishing mortality age effect (s) for age 1 have been fixed to 1. In a4a this could not be done so results have been rescaled.

Again, similar patterns are observed with increasing probability intervals for last ages and years. For the bayesian run these two sets of parameter show some correlation, negative between age and year factors and positive among the sets.

```
par(mfrow = c(2, 1))
plot(bfyear[2, ], type = "l", ylim = c(0, 0.5), main = "f year",
    xlab = "years", ylab = "f", col = 2)
lines(c(bfyear[1, ]), lty = 2, col = 2)
lines(c(bfyear[3, ]), lty = 2, col = 2)
lines(c(a4afyear[1, ]), lty = 2, col = 3)
lines(c(a4afyear[3, ]), lty = 2, col = 3)
lines(c(a4afyear[2, ]), lty = 1, col = 3)
lines(c(a4asimfyear[1, ]), lty = 2, col = 4)
lines(c(a4asimfyear[3, ]), lty = 2, col = 4)
lines(c(a4asimfyear[2, ]), lty = 1, col = 4)
legend("topleft", legend = (c("Bayes", "a4aMC", "a4aSIM")), lty = 1,
    col = c(2:4))
plot(bsage[2, ], type = "l", ylim = c(0, 5), main = "s age",
    xlab = "age", ylab = "s", col = 2)
lines(c(bsage[1, ]), lty = 2, col = 2)
lines(c(bsage[3, ]), lty = 2, col = 2)
lines(c(a4asage[1, ]), lty = 2, col = 3)
lines(c(a4asage[3, ]), lty = 2, col = 3)
lines(c(a4asage[2, ]), lty = 1, col = 3)
lines(c(a4asimsage[1, ]), lty = 2, col = 4)
lines(c(a4asimsage[3, ]), lty = 2, col = 4)
lines(c(a4asimsage[2, ]), lty = 1, col = 4)
legend("topleft", legend = (c("Bayes", "a4aMC", "a4aSIM")), lty = 1,
    col = c(2:4))
```

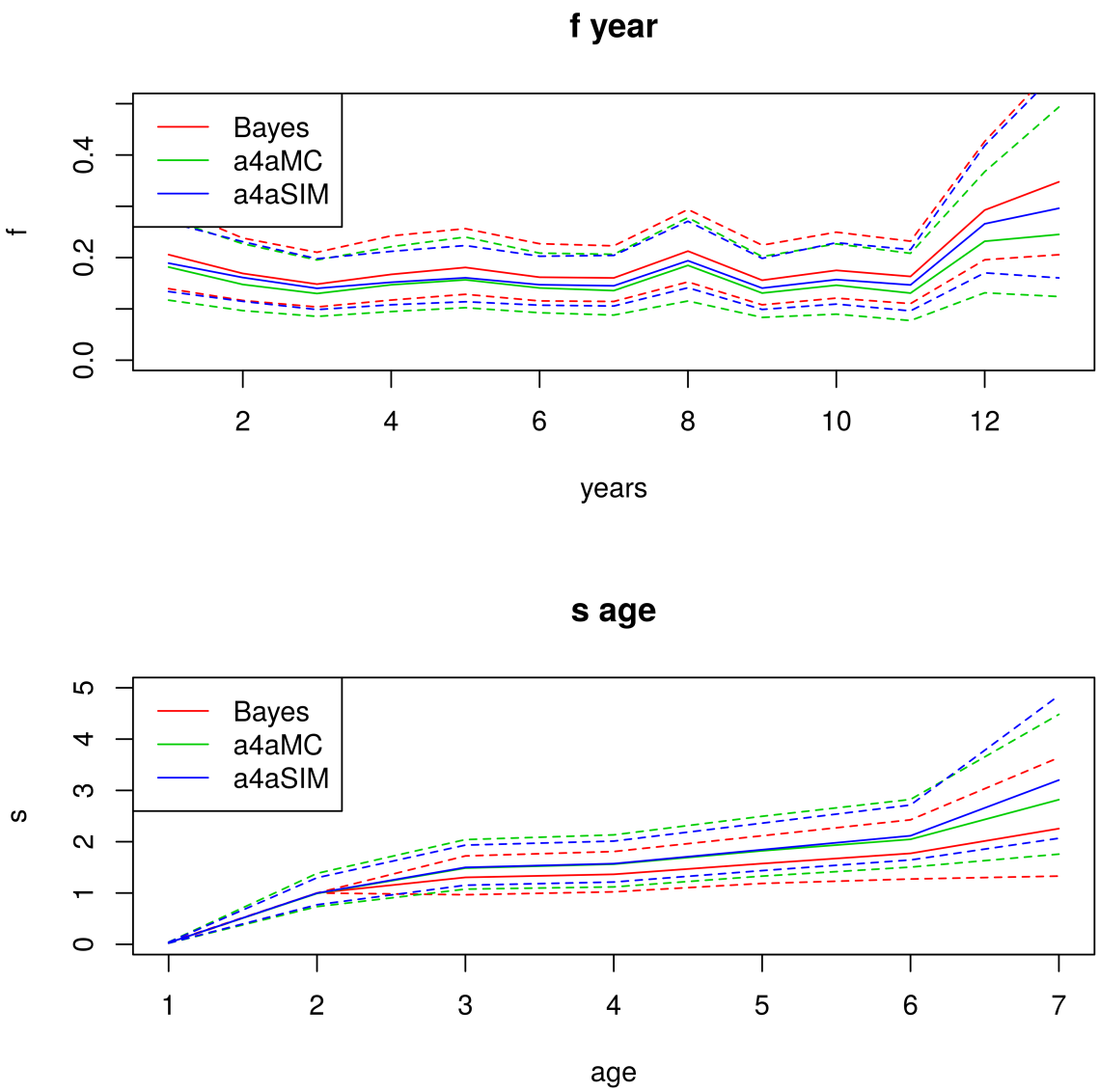

Figure 145: Fishing mortality age and year effecs for each method

The variance parameter estimate for the catch observation equation is lower and more precise in the a4a SIMULATE run, although for the rest of the parameters the Bayesian run results present less variability. There are not big differences except for the DEPM survey catchability parameter, for which a4a tends to estimate higher values with more variability.

```
par(mfrow = c(2, 3))
# C
plot(density(1/(b_output[, "tau.C"])), xlim = c(0, 1), ylim = c(0,
    15), main = "C var", xlab = "var", col = 2)
lines(density((predict(a4a.MC)$vmodel[[1]][1, 1])^2), col = 3)
lines(density((predict(a4a.SIM)$vmodel[[1]][1, 1])^2), col = 4)
# curve(dinvgamma(x,dat$a.C,dat$b.C),lty=2,col=2,add=T)
legend("topright", legend = (c("Bayes", "a4aMC", "a4aSIM")),
    lty = 1, col = c(2:4))
# I
plot(density(1/unlist(b_output[, "tau.Iac"])), xlim = c(0, 1),
    ylim = c(0, 7), main = "Acoustic surv var", xlab = "var",
```

```
    col = 2)
lines(density((predict(a4a.MC)$vmodel[[2]][1, 1])^2), col = 3)
lines(density((predict(a4a.SIM)$vmodel[[2]][1, 1])^2), col = 4)
# curve(dinvgamma(x,dat$a.Iac,dat$b.Iac),lty=2,col=2,add=T)
legend("topright", legend = (c("Bayes", "a4aMC", "a4aSIM")),
    lty = 1, col = c(2:4))
# I
plot(density(1/unlist(b_output[, "tau.Idepm"])), xlim = c(0,
    1), main = "DEPM surv var", xlab = "var", col = 2)
lines(density((predict(a4a.MC)$vmodel[[3]][1, 1])^2), col = 3)
lines(density((predict(a4a.SIM)$vmodel[[3]][1, 1])^2), col = 4)
# curve(dinvgamma(x,dat$a.Idepm,dat$b.Idepm),lty=2,col=2,add=T)
legend("topright", legend = (c("Bayes", "a4aMC", "a4aSIM")),
    lty = 1, col = c(2:4))
# q
plot(density(unlist(b_output[, "qac"])), xlim = c(0, 10), main = "Acoustic surv q",
    xlab = "q", col = 2)
lines(density((predict(a4a.MC)$qmodel[[1]][1, 1])), col = 3)
lines(density((predict(a4a.SIM)$qmodel[[1]][1, 1])), col = 4)
# curve(dlnorm(x,dat$logmu.qac,sqrt(1/dat$tau.qac)),lty=2,col=2,add=T)
legend("topright", legend = (c("Bayes", "a4aMC", "a4aSIM")),
    lty = 1, col = c(2:4))
# q
plot(density(unlist(b_output[, "qdepm"])), xlim = c(0, 130),
    main = "DEPM surv q", xlab = "q", col = 2)
lines(density((predict(a4a.MC)$qmodel[[2]][1, 1])), col = 3)
lines(density((predict(a4a.SIM)$qmodel[[2]][1, 1])), col = 4)
# curve(dlnorm(x,dat$logmu.qdepm,sqrt(1/dat$tau.qdepm)),lty=2,col=2,add=T)
legend("topright", legend = (c("Bayes", "a4aMC", "a4aSIM")),
    lty = 1, col = c(2:4))
```

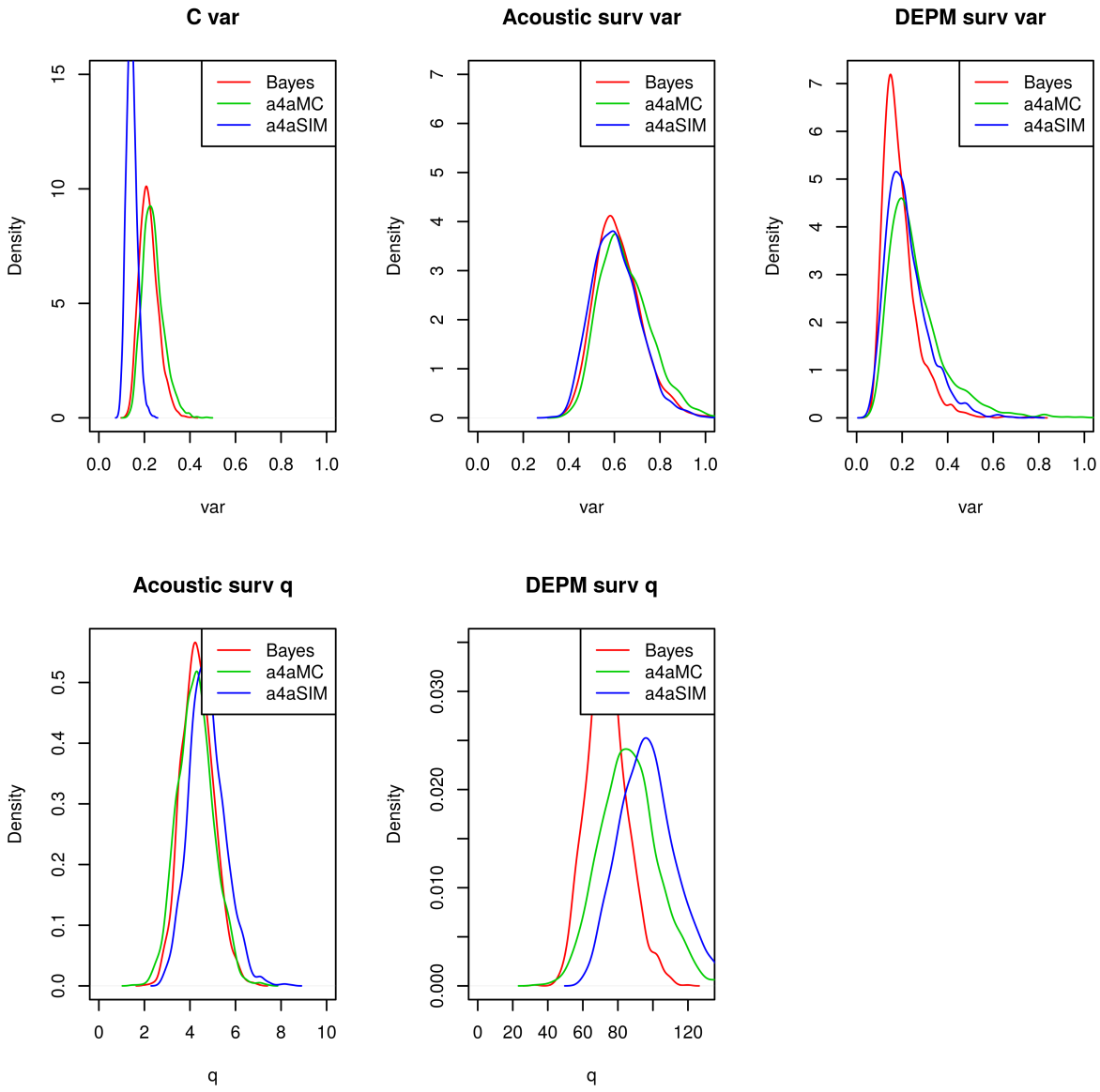

Figure 146: Catch, indices of abundance and survey's catchability for each method

Residuals do not show differences, they are ploted as medians with 90% probability intervals.

```
ggplot(resC, aes(year, median)) + geom_line(aes(year, median,
    colour = run), size = 1) + geom_ribbon(aes(y = median, ymin = q1,
    ymax = q3, fill = run), alpha = 0.2) + geom_abline(intercept = 0,
    slope = 0) + facet_grid(age ~ ., margins = F, scales = "fixed") +
    theme(legend.position = "bottom")
```

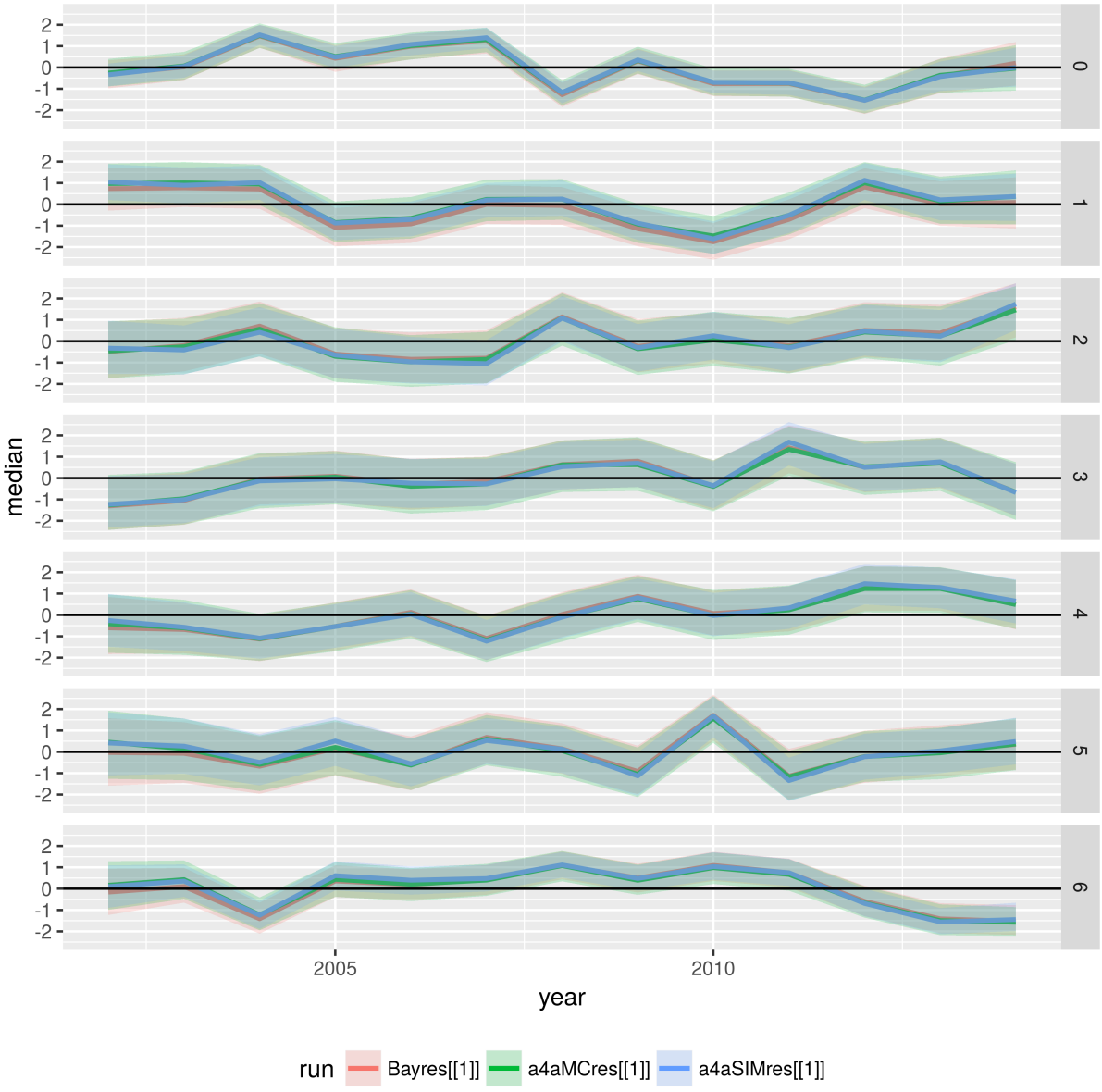

Figure 147: Cacth residuals by method

```
ggplot(resIac, aes(year, median)) + geom_line(aes(year, median,
    colour = run), size = 1) + geom_ribbon(aes(y = median, ymin = q1,
    ymax = q3, fill = run), alpha = 0.2) + geom_abline(intercept = 0,
    slope = 0) + facet_grid(age ~ ., margins = F, scales = "fixed") +
    theme(legend.position = "bottom")
```

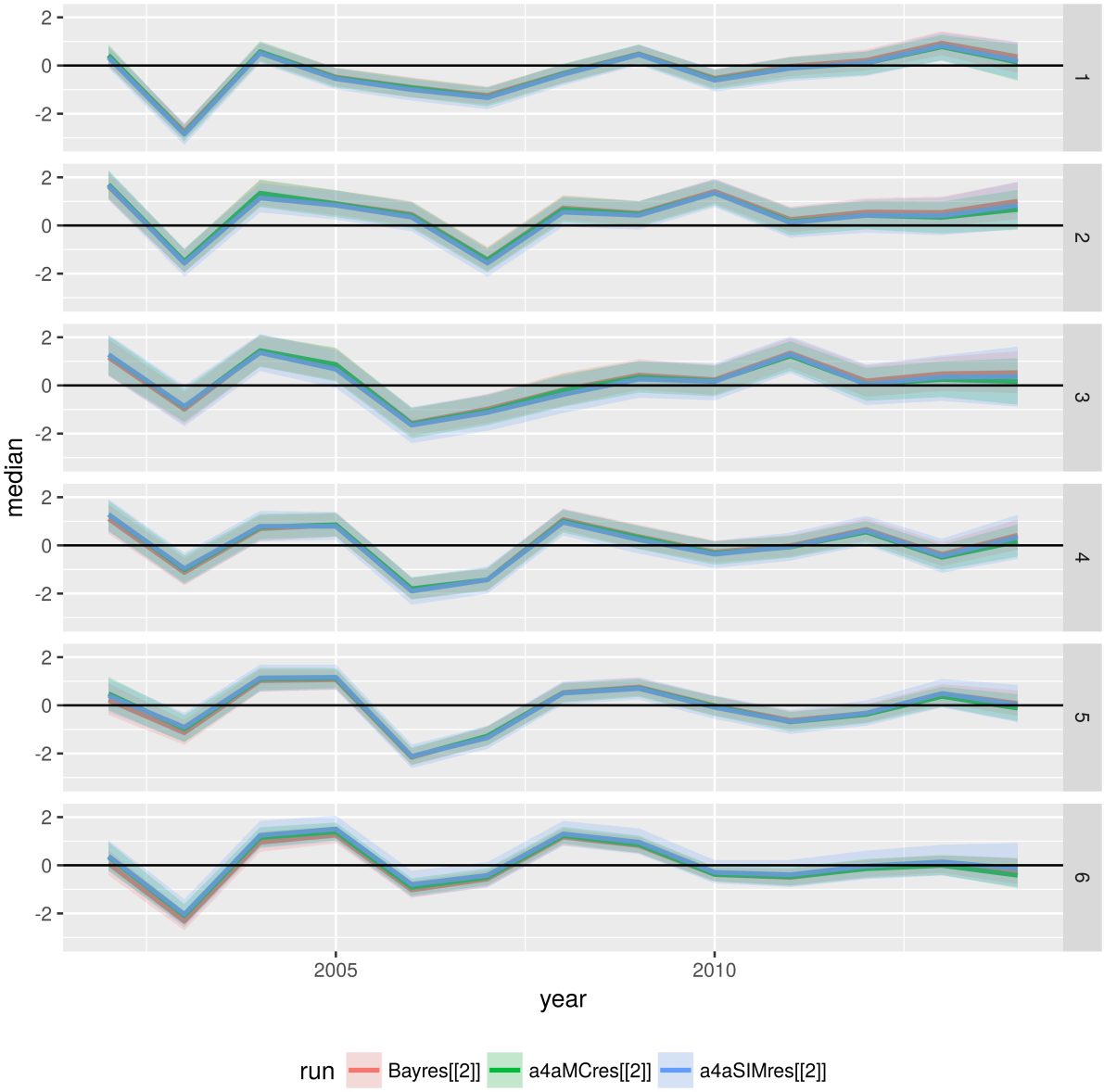

Figure 148: Acoustic survey index residuals by method

```
ggplot(resIdepm, aes(year, median)) + geom_line(aes(year, median,
    colour = run), size = 1) + geom_ribbon(aes(y = median, ymin = q1,
    ymax = q3, fill = run), alpha = 0.2) + geom_abline(intercept = 0,
    slope = 0) + facet_grid(age ~ ., margins = F, scales = "fixed") +
    theme(legend.position = "bottom")
```

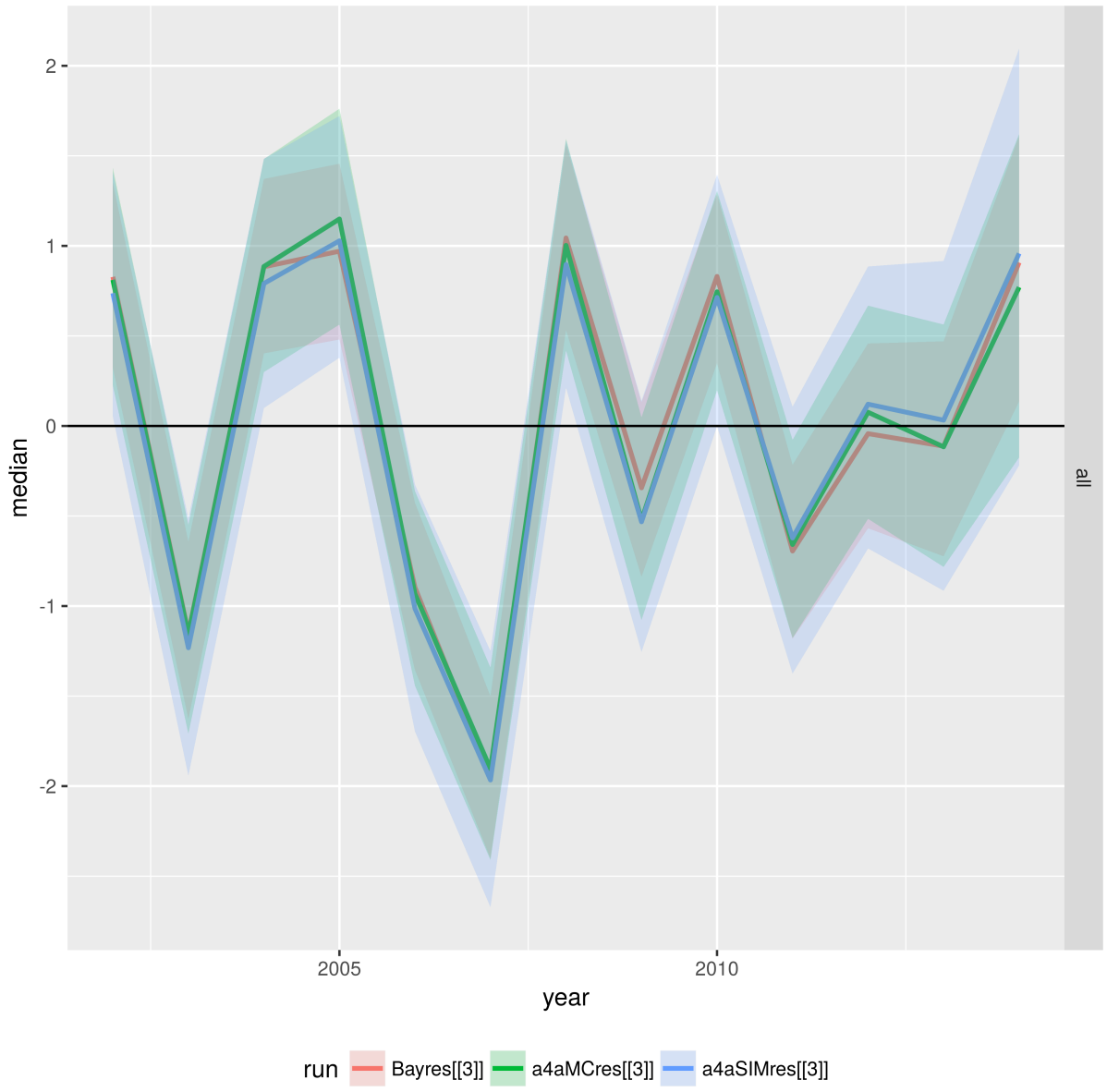

Figure 149: DEPM survey index residuals by method

Other parameters also seem very similar:

```
ggtail <- "+geom_line(aes(year,median,colour = run),size=1) +
\tgeom_ribbon(aes(y = median, ymin = q1, ymax = q3, fill = run),alpha = 0.2) +
\tgeom_abline(intercept=0,slope=0) +
\tfacet_grid(age ~ ., margins = F, scales = \"free\") +
\ttheme(legend.position = \"bottom\")"
eval(parse(text = paste("ggplot(Ns, aes(year, median))", ggtail,
    sep = "")))
```

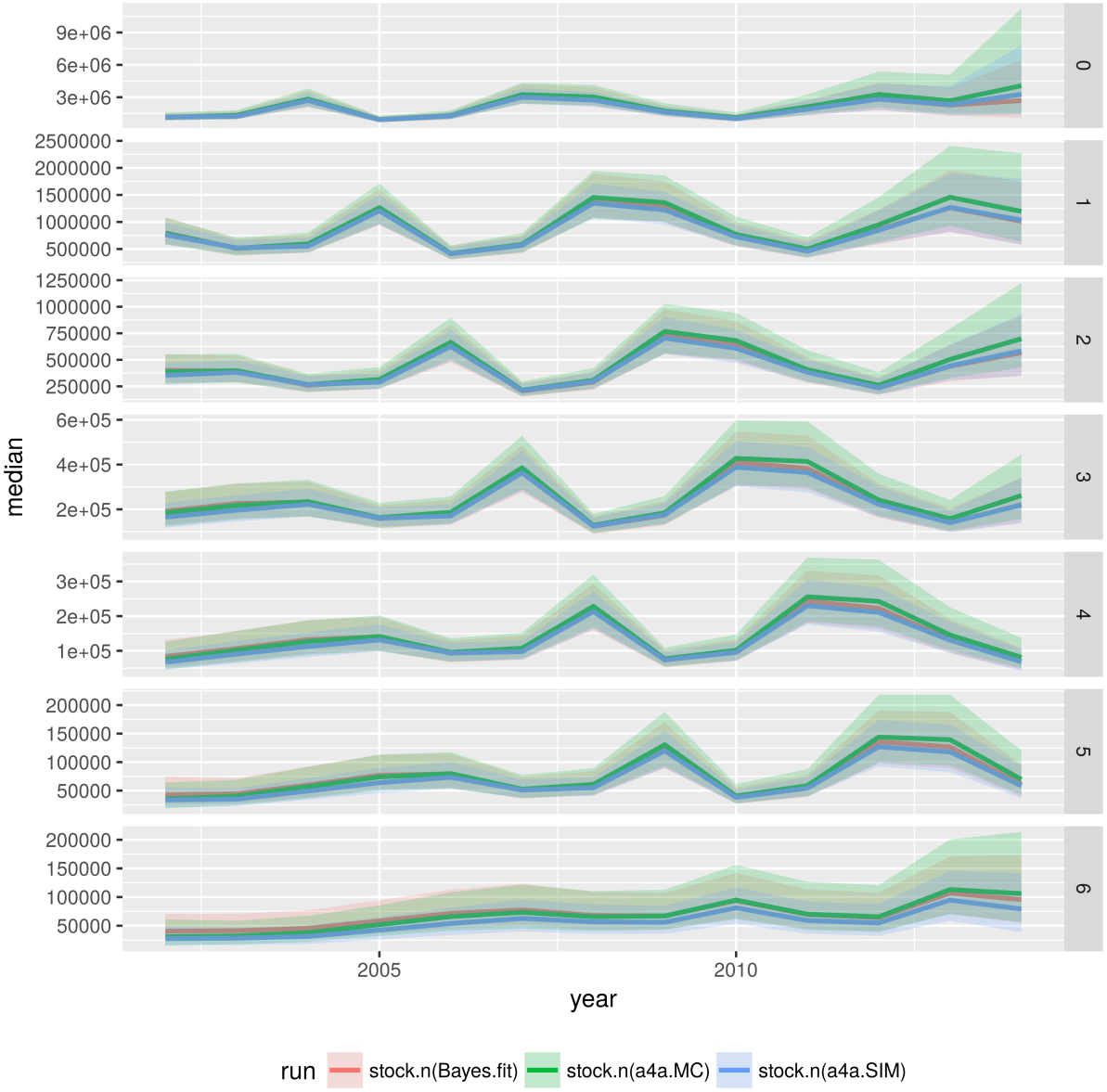

Figure 150: Stock abundance at age by method

```
eval(parse(text = paste("ggplot(SSBs, aes(year, median))", ggtail,
    sep = "")))
```

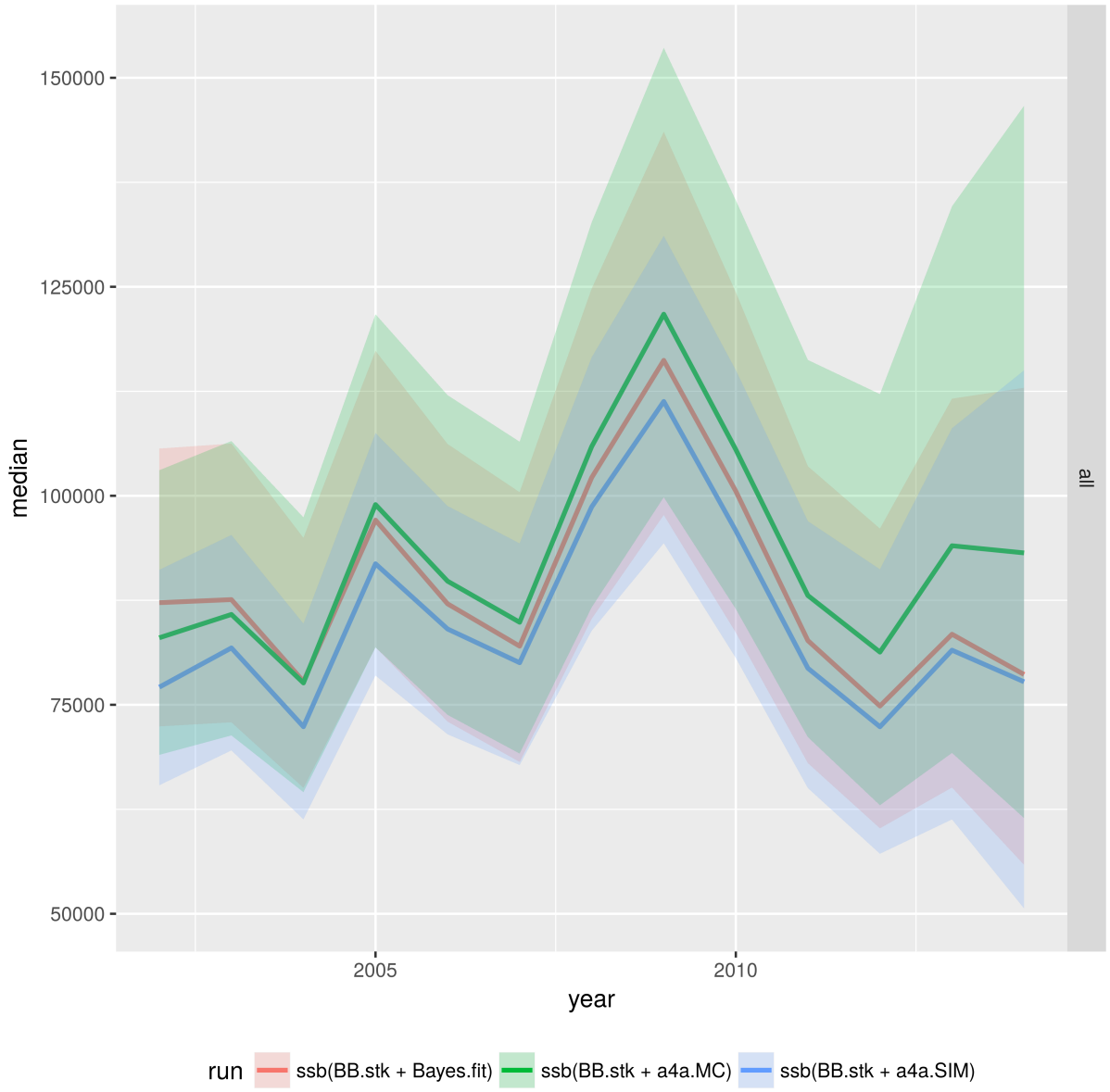

Figure 151: SSB by method

```
eval(parse(text = paste("ggplot(Cs, aes(year, median))", ggtail,
    sep = "")))
```

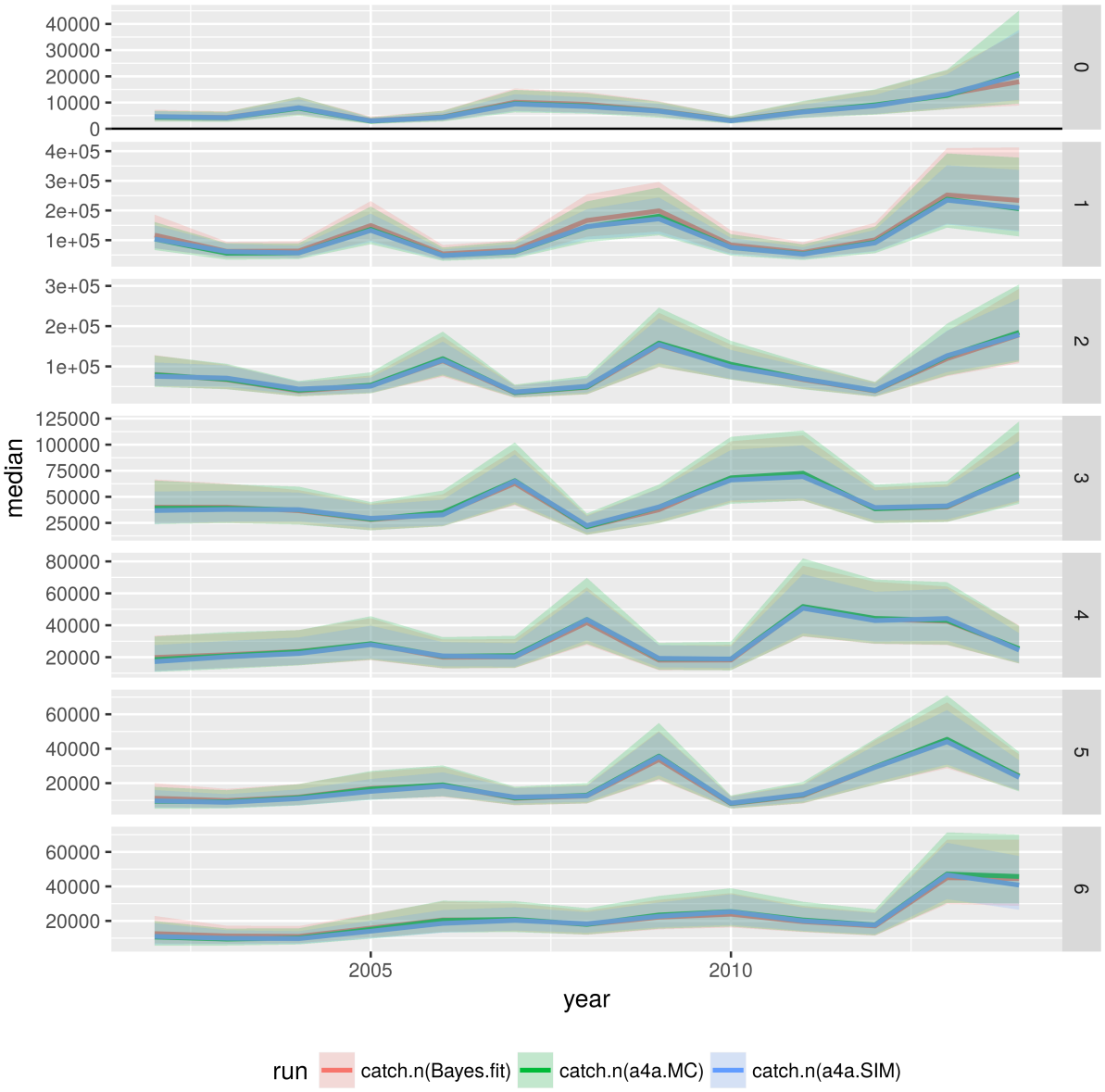

Figure 152: Cacth by method

```
eval(parse(text = paste("ggplot(Fs, aes(year, median))", ggtail,
    sep = "")))
```

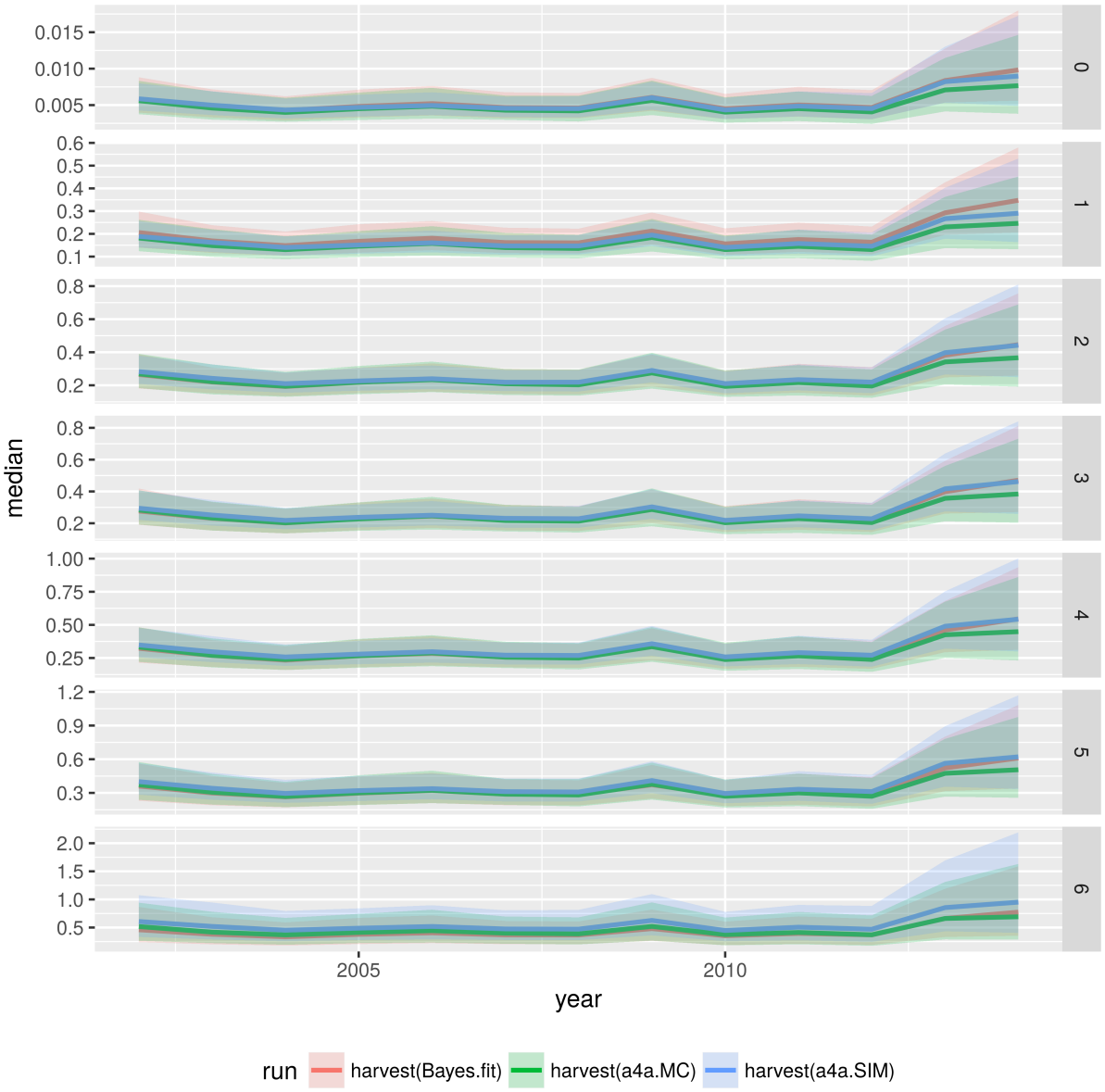

Figure 153: Fishing mortality by method

```
eval(parse(text = paste("ggplot(recs, aes(year, median))", ggtail,
    sep = "")))
```

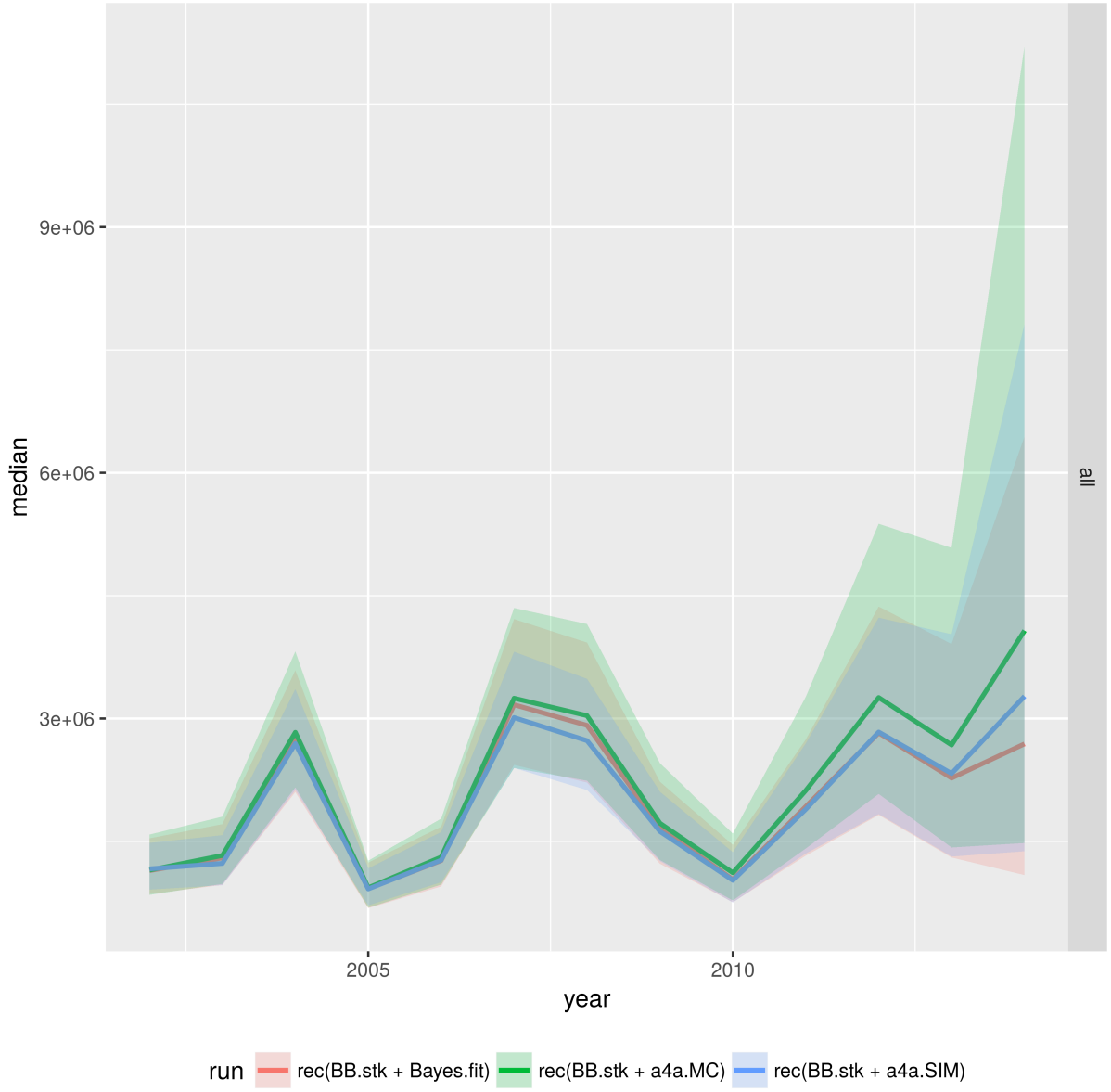

Figure 154: Recruitment by method

```
eval(parse(text = paste("ggplot(Iac, aes(year, median))", ggtail,
    sep = "")))
```

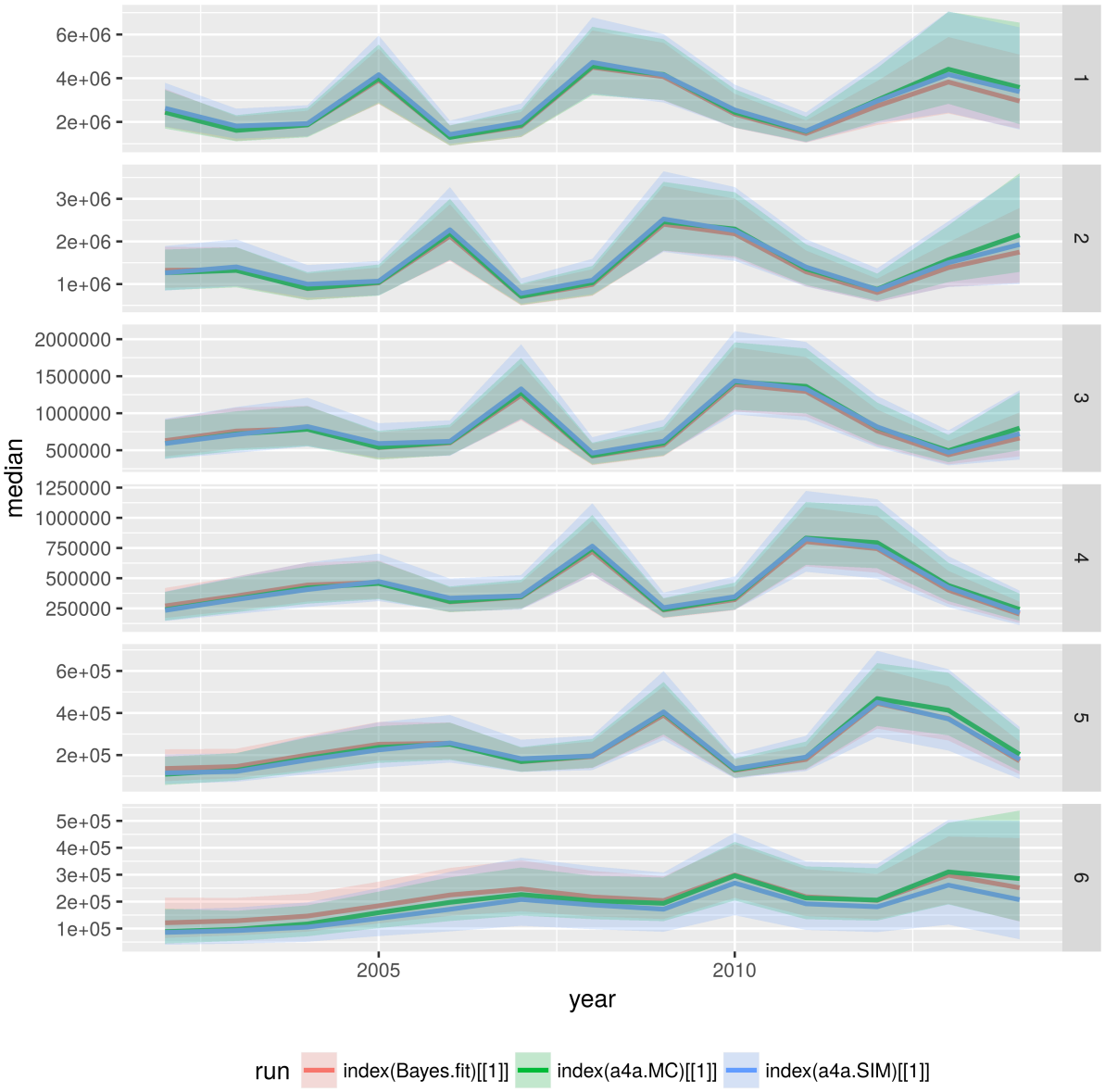

Figure 155: Acustic survey index by method

```
eval(parse(text = paste("ggplot(Idepm, aes(year, median))", ggtail,
    sep = "")))
```

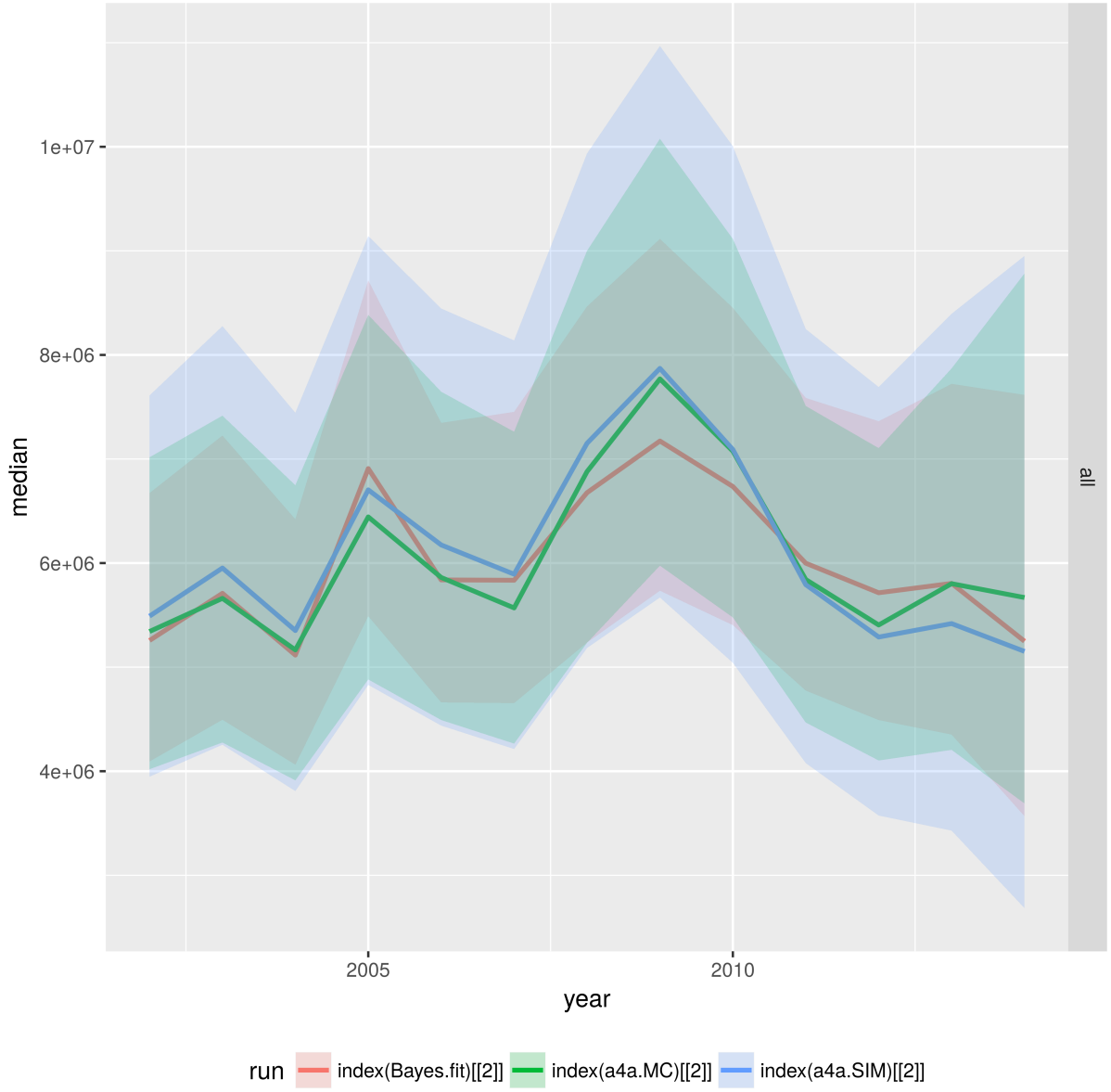

Figure 156: DEPM survey index by method

Cross correlation patterns show that fishing mortality year effect factors are correlated in both cases, meanwhile the age effect factors present correlation for the Bayesian run, this could be due to the fact that one of the parameters was fixed. Catchability parameters show correlations with fishing mortality factors as well. In the a4a MCMC run, recruitment and n1 submodels are defined with an intercept which is correlated with the rest of the parameters, something that does not happen in the Bayesian approach given that intercepts are not used.

In the a4a SIMULATE run we cannot see the correlation between stk model parameters, qmodel parameters and vmodel parameters given that simulations are done independently, without taking into account the complete covariance matrix from the hessian (simulate-methods.R).

```
print(levelplot(cor(coda::as.mcmc(b_output[, sel_params])), col.regions = rainbow(1000)[600:1],
    cuts = 100, at = seq(-1, 1, length.out = 600), scales = list(x = list(rot = 90))))
```

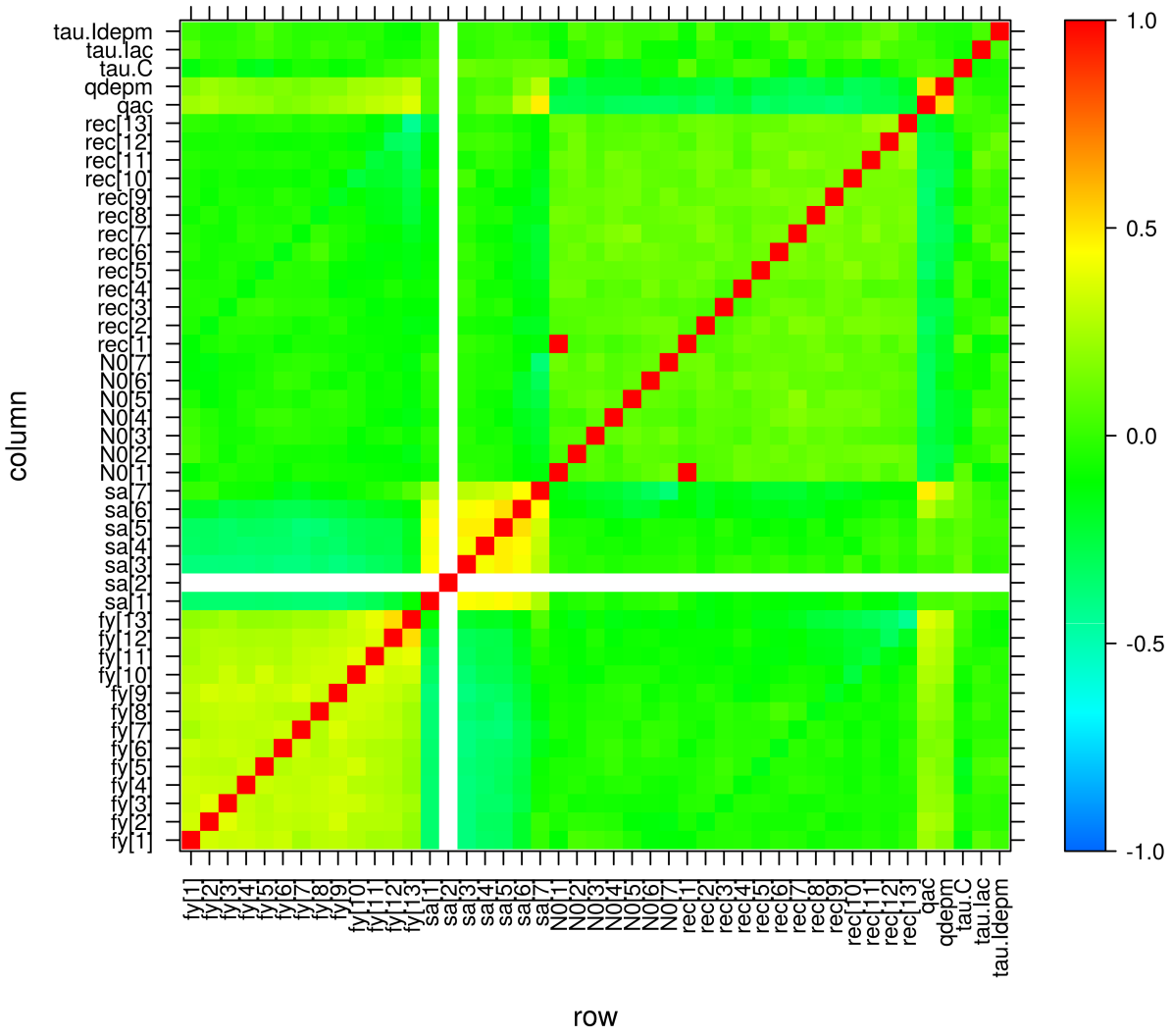

Figure 157: Absolute correlation across parameters. Bayesian method.

```
plot(a4a.MC)
```

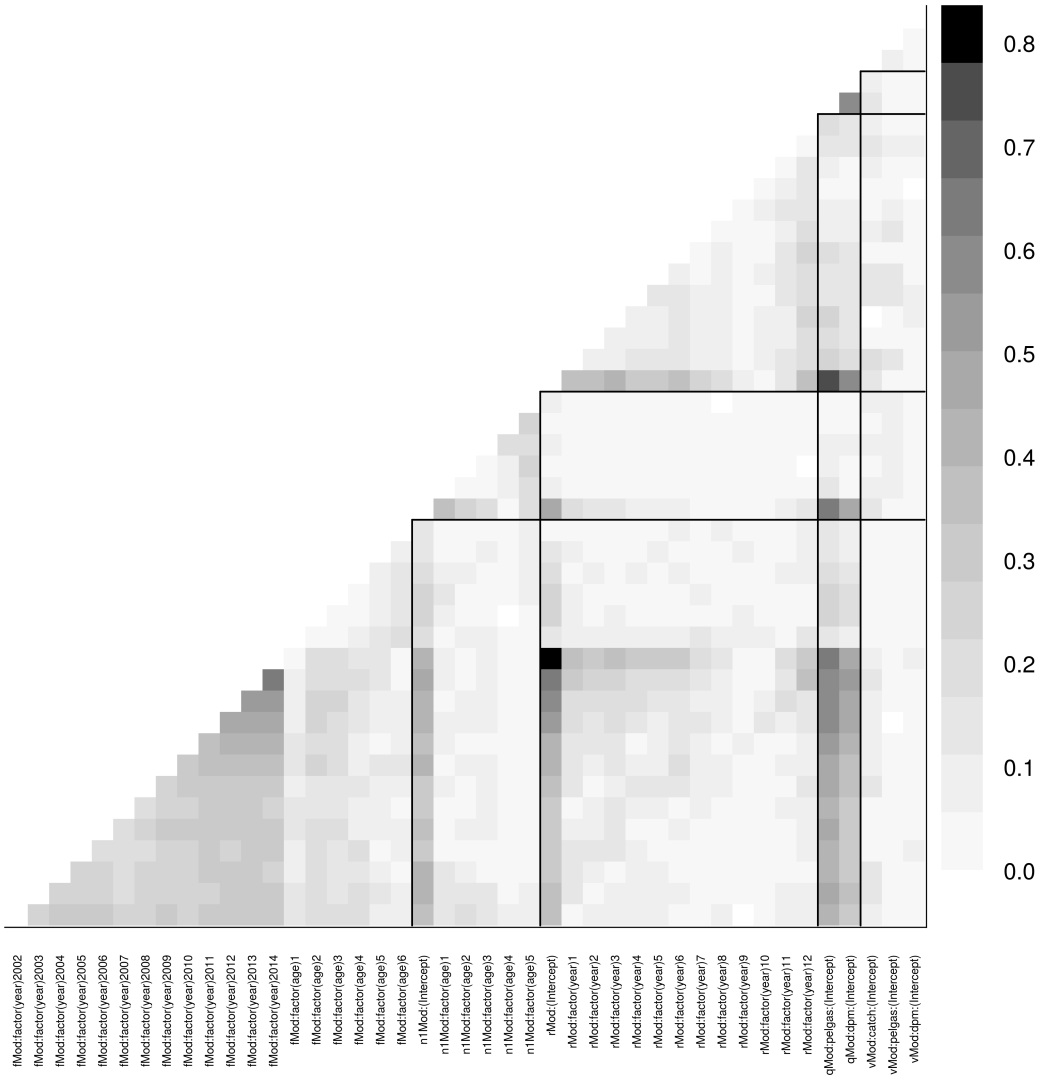

Figure 158: Absolute correlation across parameters. MCMC method.

```
print(levelplot(cor(coda::as.mcmc(a4a.SIMobj)), col.regions = rainbow(1000)[600:1],
    cuts = 100, at = seq(-1, 1, length.out = 600), scales = list(x = list(rot = 90))))
```

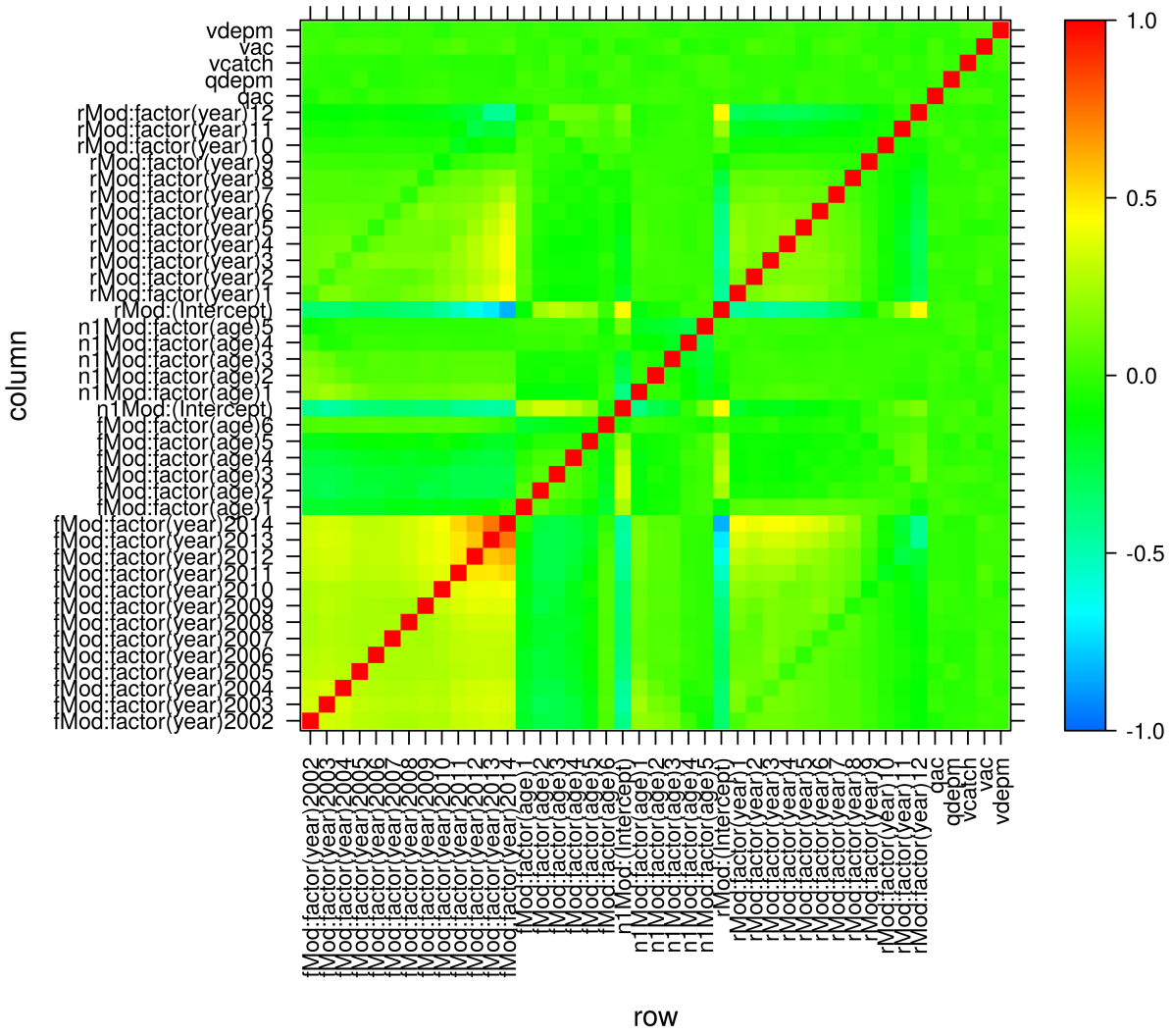

Figure 159: Absolute correlation across parameters. Stochastic method.

```
print(acfplot(coda::as.mcmc(b_output[, sel_params]), ylim = c(-1,
    1), par.strip.text = list(cex = 0.7)))
```

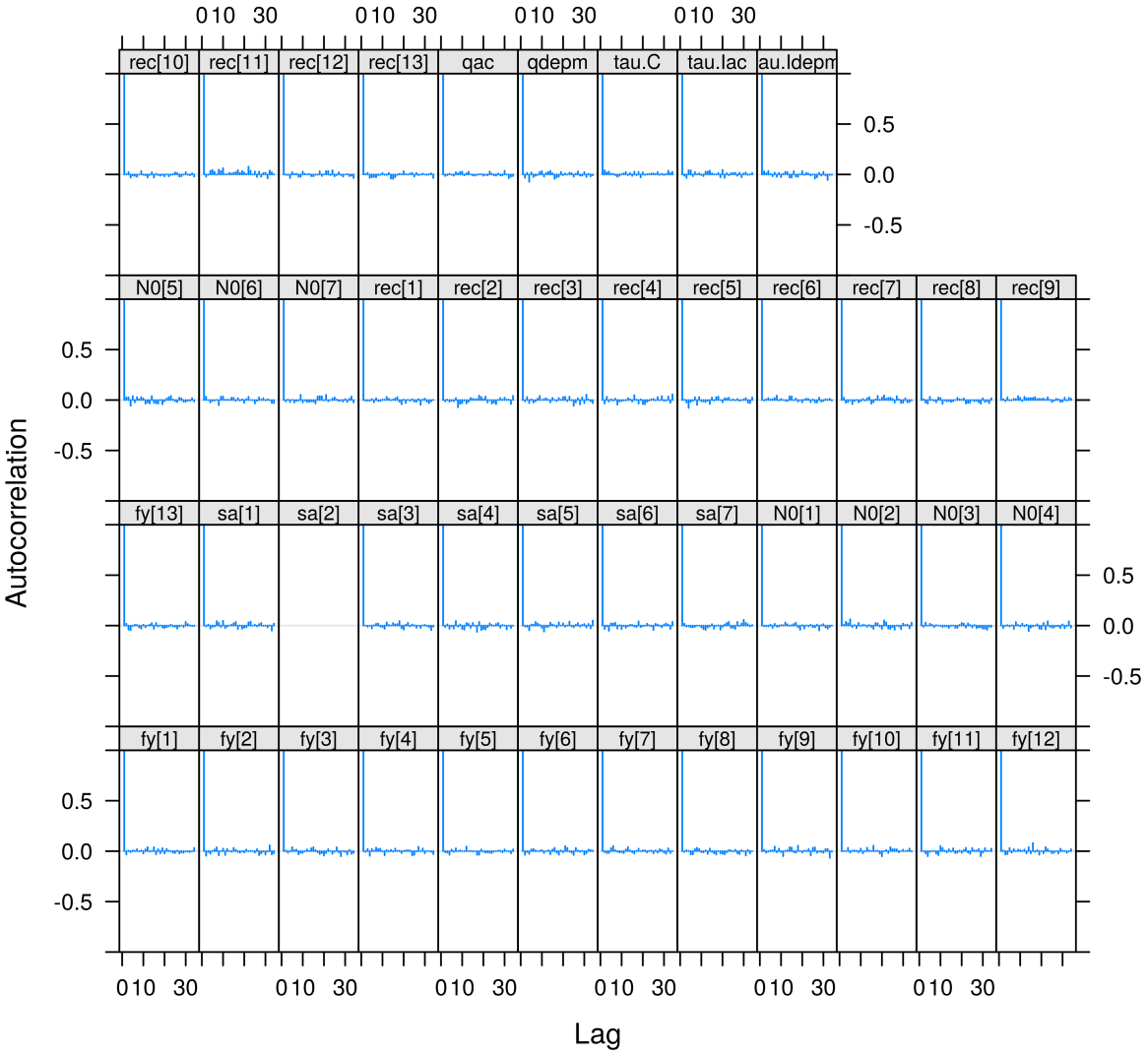

Figure 160: Auto-correlation. Bayesian method.

```
print(acfplot(as.mcmc(a4a.MC), ylim = c(-1, 1), par.strip.text = list(cex = 0.7)))
```

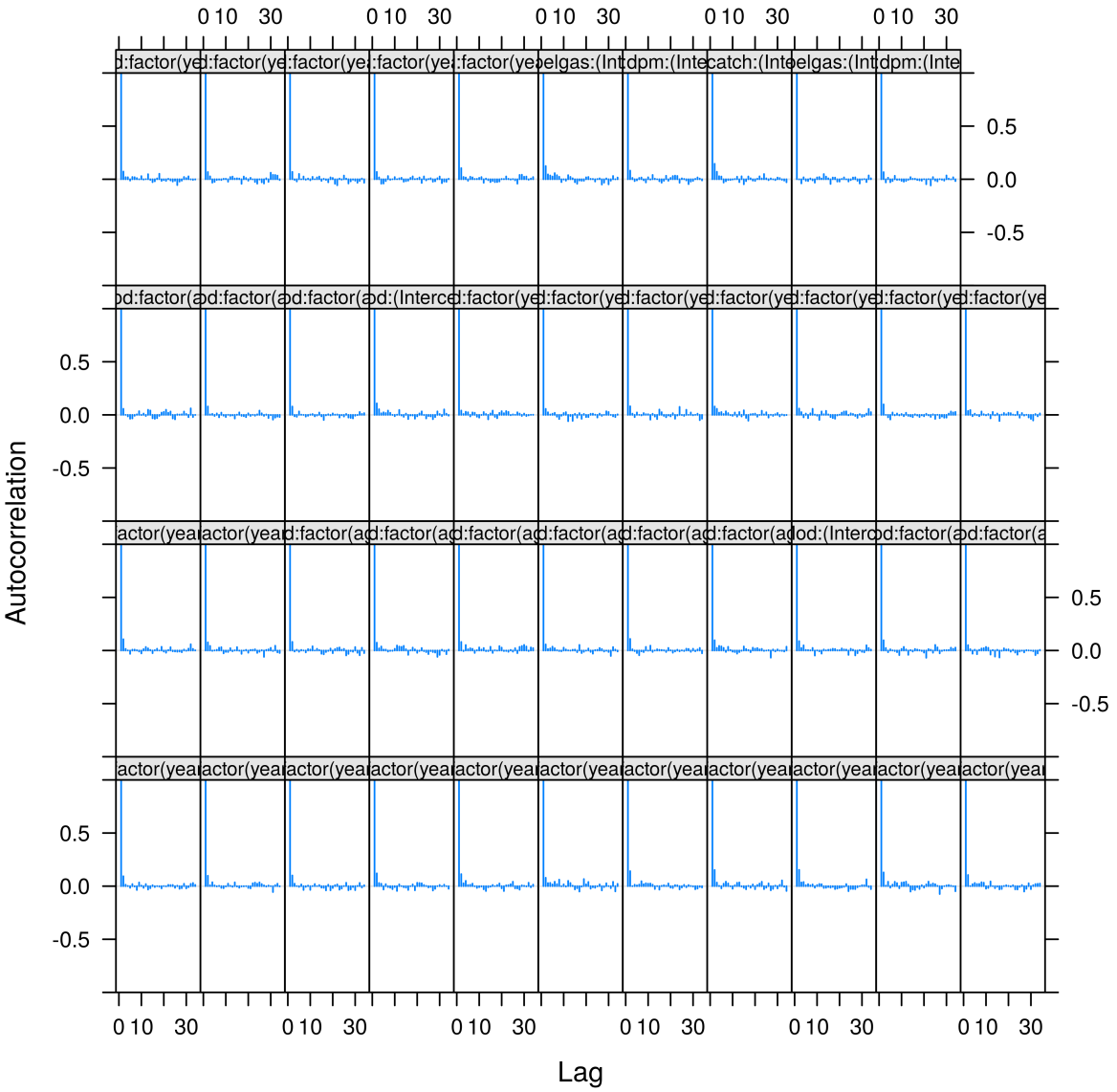

Figure 161: Auto-correlation. MCMC method.

```
print(acfplot(coda::as.mcmc(a4a.SIMobj), ylim = c(-1, 1), par.strip.text = list(cex = 0.7)))
```

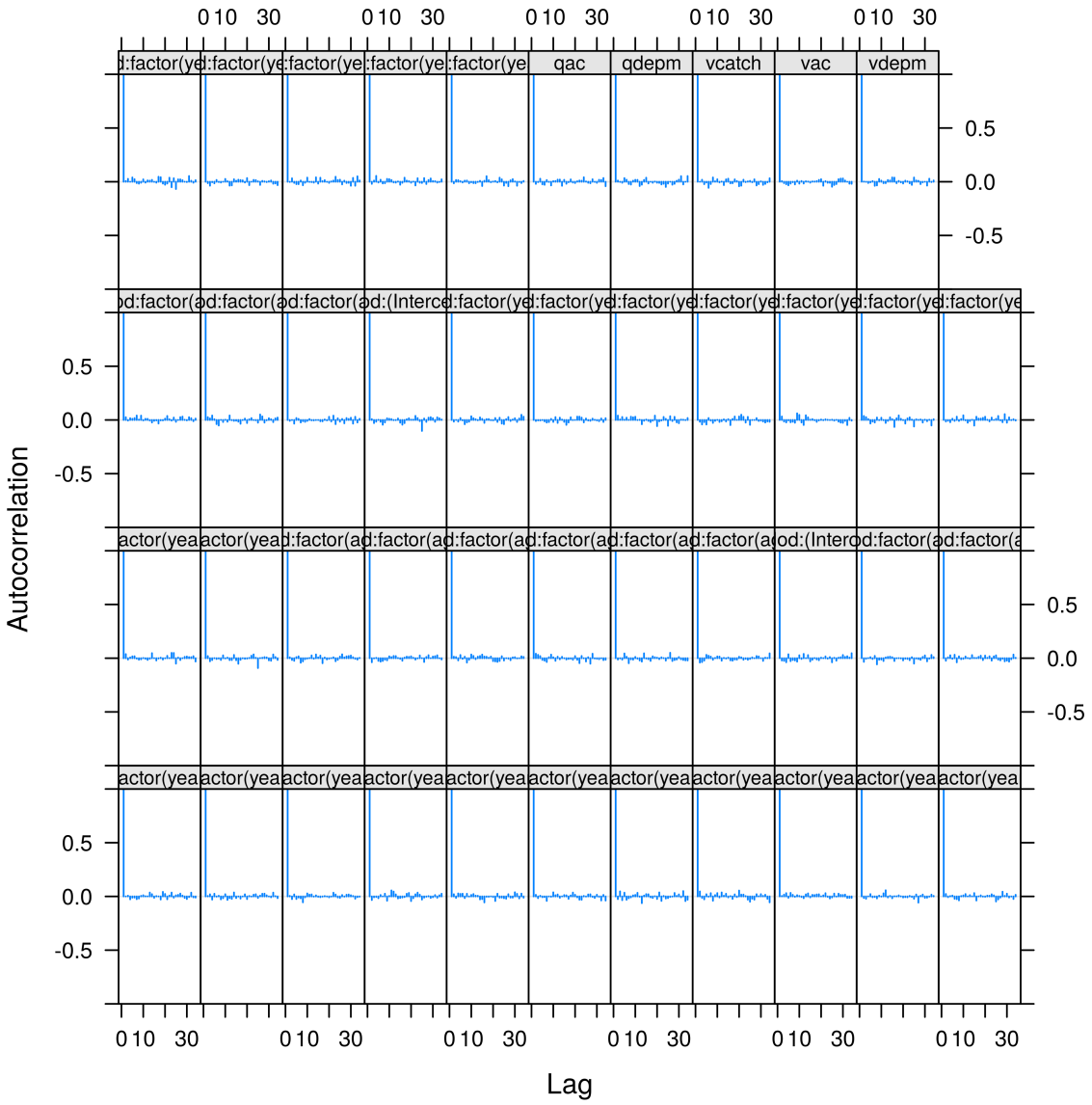

Figure 162: Auto-correlation. Stochastic (?) method.

7. Results and final comments

The a4a assessment mimicked the overall trends of SSB, R and F of the SS3 Iberian sardine assessment. Some differences were found in the first years of the time series. These differences might be due to selectivity assumptions: in SS3, selectivity-at-age was assumed to vary smoothly over time until 1991 and be constant thereafter, whereas in aa, the fishing mortality model assumed a constant selectivity-at-age over the whole assessment period.

A visual evaluation of the consistency between the spatial hypothesis S1 and S2 can be done based on the SSB estimates. Figure 163 shows that both trends are remarkably similar until 2012, when they start to diverge. In 2012 the Iberian stock (sub-units NW and S) was at a very low level and the migration rates between the Iberian and the Bay of Biscay sub-units may have increased. In such case, the stock assessment model assumption of closed population is less likely to be maintained and the two estimates of SSB diverge.

Note that the sub-unit's trends shown in this section should be viewed with caution since area-disaggregated data needs to be revised.

```
A.stks <- FLStocks(q1 = A.q1smc, q2 = A.q2smc, q3 = A.q3smc,
    q4 = A.q4smc)
BB.stks <- FLStocks(q1 = BB.q1smc, q2 = BB.q2smc, q3 = BB.q3smc,
    q4 = BB.q4smc)
S.stks <- FLStocks(q1 = S.q1smc, q2 = S.q2smc, q3 = S.q3smc,
    q4 = S.q4smc)
NW.stks <- FLStocks(q1 = NW.q1smc, q2 = NW.q2smc, q3 = NW.q3smc,
    q4 = NW.q4smc)

A.ssb <- lapply(A.stks, ssb)
BB.ssb <- lapply(BB.stks, ssb)
S.ssb <- lapply(S.stks, ssb)
NW.ssb <- lapply(NW.stks, ssb)

SSB <- list()
length(SSB) <- length(A.ssb)
q1.ssb <- FLQuants(A = ssb(A.q1smc)/1000, BB = ssb(BB.q1smc)/1000,
    S = ssb(S.q1smc), NW = ssb(NW.q1smc))
q2.ssb <- FLQuants(A = ssb(A.q2smc)/1000, BB = ssb(BB.q2smc)/1000,
    S = ssb(S.q2smc), NW = ssb(NW.q2smc))
q3.ssb <- FLQuants(A = ssb(A.q3smc)/1000, BB = ssb(BB.q3smc)/1000,
    S = ssb(S.q3smc), NW = ssb(NW.q3smc))
q4.ssb <- FLQuants(A = ssb(A.q4smc)/1000, BB = ssb(BB.q4smc)/1000,
    S = ssb(S.q4smc), NW = ssb(NW.q4smc))

for (i in 1:length(A.ssb)) {
    SSB[[i]] <- FLQuants(A = A.ssb[[i]]/1000, `Sub-units` = S.ssb[[i]][,
        ac(2002:2014)] + NW.ssb[[i]][, ac(2002:2014), , , , 1:50] +
        BB.ssb[[i]][, ac(2002:2014)]/1000)
}
```

```
pr <- c(0.1, 0.5, 0.9)
flqs <- SSB[[2]]
flqs <- lapply(flqs, quantile, probs = pr)
df0 <- as.data.frame(flqs)
df0$stats <- "SSB"
df0 <- dcast(df0, age + year + unit + season + area + qname +
    stats ~ iter, value.var = "data")


## Error in eval(expr, envir, enclos):  could not find function "dcast"


p <- ggplot(data = df0, aes(x = as.factor(year), y = `50%`, group = qname)) +
    facet_grid(stats ~ ., scales = "free") + geom_line(aes(colour = qname),
```

```
    na.rm = T, colour = "black") + scale_fill_manual(values = c("gray60",
    "gray80")) + xlab("") + ylab("") + expand_limits(y = 0) +
    theme(legend.title = element_blank(), legend.text = element_text(size = 14),
        panel.background = element_blank(), strip.text.x = element_text(size = 18),
        axis.line = element_line(colour = "black"), panel.border = element_rect(colour = "black",
            fill = NA)) + geom_ribbon(aes(x = as.factor(year),
    ymin = `10%`, ymax = `90%`, group = qname, colour = qname,
    fill = qname), alpha = 0.5, linetype = 0, na.rm = T, colour = "black")
```

```
## Error in eval(expr, envir, enclos): object '50%' not found
```

Figure 163: SSB estimates and 80% confidence intervals for the overall stock assessment (A) and the sub-units aggregation (Sub-units)

One of the advantages of the approach proposed is to make it possible to look into sub-units of the stock with regards to their productivity and exploitation. Figure 164 shows the time series of fishing mortality that each sub-unit was exposed to and Figure 165 shows the time series of recruitment by sub-unit.

```
A.fb <- lapply(A.stks, fbar)
BB.fb <- lapply(BB.stks, fbar)
S.fb <- lapply(S.stks, fbar)
NW.fb <- lapply(NW.stks, fbar)

pr <- c(0.1, 0.5, 0.9)
flqs <- FLQuants(BB = BB.fb[[2]], NW = NW.fb[[2]], S = S.fb[[2]])
flqs <- lapply(flqs, quantile, probs = pr)
df0 <- as.data.frame(flqs)
df0$stats <- "Fbar"
df0 <- dcast(df0, age + year + unit + season + area + qname +
    stats ~ iter, value.var = "data")


## Error in eval(expr, envir, enclos):  could not find function "dcast"


p <- ggplot(data = df0, aes(x = as.factor(year), y = `50%`, group = qname)) +
    facet_grid(stats ~ ., scales = "free") + geom_line(aes(colour = qname),
    na.rm = T, colour = "black") + scale_fill_manual(values = c("gray80",
    "gray70", "gray60")) + xlab("") + ylab("") + expand_limits(y = 0) +
    theme(legend.title = element_blank(), legend.text = element_text(size = 14),
        panel.background = element_blank(), strip.text.x = element_text(size = 18),
        axis.line = element_line(colour = "black"), panel.border = element_rect(colour = "black",
            fill = NA), axis.text.x = element_text(angle = 90,
            vjust = 0.5)) + geom_ribbon(aes(x = as.factor(year),
    ymin = `10%`, ymax = `90%`, group = qname, colour = qname,
    fill = qname), alpha = 0.5, linetype = 0, na.rm = T, colour = "black")
```

```
## Error in eval(expr, envir, enclos):  object '50%' not found
```

Figure 164: Fishing mortality estimates and 80% confidence intervals for each sub-unit

```
A.r <- lapply(A.stks, rec)
BB.r <- lapply(BB.stks, rec)
S.r <- lapply(S.stks, rec)
NW.r <- lapply(NW.stks, rec)

pr <- c(0.1, 0.5, 0.9)
flqs <- FLQuants(BB = BB.r[[2]]/1000, NW = NW.r[[2]], S = S.r[[2]])
flqs <- lapply(flqs, quantile, probs = pr)
df0 <- as.data.frame(flqs)
df0$stats <- "Recruitment"
df0 <- dcast(df0, age + year + unit + season + area + qname +
    stats ~ iter, value.var = "data")

## Error in eval(expr, envir, enclos):  could not find function "dcast"

p <- ggplot(data = df0, aes(x = as.factor(year), y = `50%`, group = qname)) +
```

```
    facet_grid(stats ~ ., scales = "free") + geom_line(aes(colour = qname),
    na.rm = T, colour = "black") + scale_fill_manual(values = c("gray80",
    "gray70", "gray60")) + xlab("") + ylab("") + expand_limits(y = 0) +
    theme(legend.title = element_blank(), legend.text = element_text(size = 14),
        panel.background = element_blank(), strip.text.x = element_text(size = 18),
        axis.line = element_line(colour = "black"), panel.border = element_rect(colour = "black",
            fill = NA), axis.text.x = element_text(angle = 90,
            vjust = 0.5)) + geom_ribbon(aes(x = as.factor(year),
    ymin = `10%`, ymax = `90%`, group = qname, colour = qname,
    fill = qname), alpha = 0.5, linetype = 0, na.rm = T, colour = "black")
```

```
p
```

```
## Error in eval(expr, envir, enclos): object '50%' not found
```

Figure 165: Recruitment estimates and 80% confidence intervals for each sub-unit

A more detailed look into the fleet dynamics in each sub-unit can be obtained through the inspection of fishing mortality at age. Figure 166 depicts the estimates levels of F by age

in each sub-unit.

```
A.f <- lapply(A.stks, harvest)
BB.f <- lapply(BB.stks, harvest)
S.f <- lapply(S.stks, harvest)
NW.f <- lapply(NW.stks, harvest)

flqs <- FLQuants(BB = iterMedians(BB.f[[2]]), NW = iterMedians(NW.f[[2]]),
    S = iterMedians(S.f[[2]]))
df0 <- as.data.frame(flqs)

wireframe(data ~ age + year | qname, zlab = "F", data = df0)
```

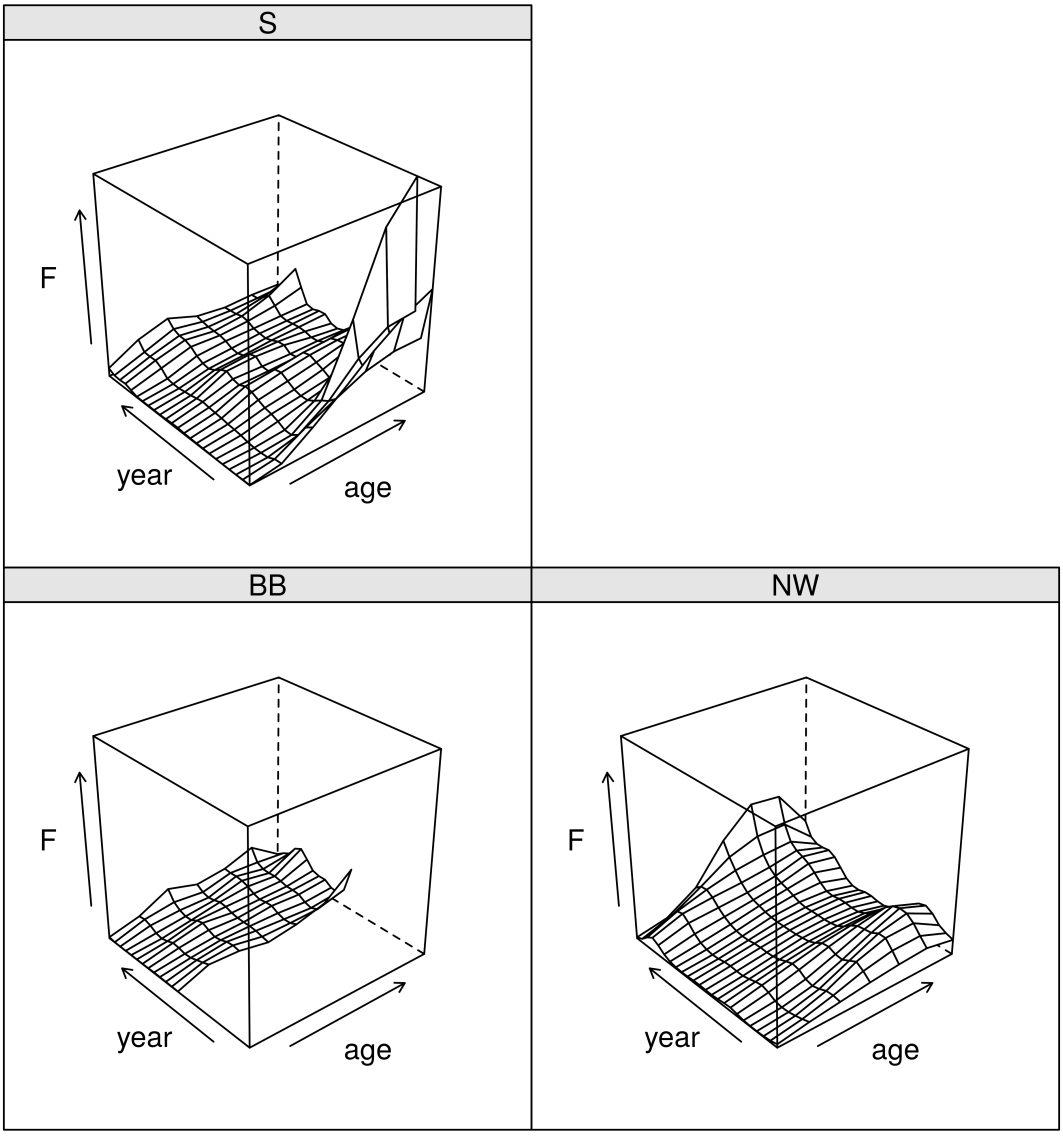

Figure 166: F-at-age estimates for each sub-unit

All references are included in the text as urls, which allow an immediate access to the documents.

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LB-NA-27841-EN-N

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doi:10.2788/890201
ISBN 978-92-79-57759-8